

GenCore version 4.5  
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# OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 21:30:32 ; Search time 2546.98 Seconds  
(without alignments)  
1764.633 Million cell updates/sec

Title: US-09-786-015-3  
Perfect score: 333  
Sequence: 1 caggatgtgcgactcagcc.....ccaggctgacgcctctcgtggt 333

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estlov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estcl:\*  
10: gb\_estc2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_low:\*  
15: em\_gss\_pin:\*  
16: em\_gss\_vrtc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	275.4	82.7	451	10	BE476752	BE476752 160141 BA
2	269	80.8	515	10	BE476398	BE476398 159628 BA
3	265.8	79.8	495	10	BE485669	BE485669 172803 BA
4	256.2	76.9	564	10	BE589073	BE589073 194817 BA
5	251.2	75.4	655	10	BE691510	BE691510 340705 BA
6	249.6	75.0	467	10	BE590205	BE590205 197215 BA
7	248.2	74.5	493	10	BE487574	BE487574 176397 BA
8	243.4	73.1	467	10	BE688999	BE688999 336848 BA
9	243.2	73.0	496	10	BE476758	BE476758 160150 BA
10	240.2	72.1	484	10	BE689524	BE689524 337633 BA
11	240	72.1	518	10	BE483566	BE483566 169766 BA
12	239.4	71.9	542	10	BE751028	BE751028 202731 MA
13	237.6	71.4	557	10	BE722165	BE722165 190280 MA
14	236.8	71.1	503	10	BE485929	BE485929 173232 BA
15	236.8	71.1	514	10	BE483616	BE483616 169632 BA
16	236.4	71.0	396	10	BE488003	BE488003 177194 BA
17	236	70.9	553	10	BE749919	BE749919 201001 MA

18	235.4	70.7	538	10	BE688590	BE688590 336269 BA
19	235.2	70.6	474	10	BE588329	BE588329 194153 BA
20	235.2	70.6	477	10	BE690381	BE690381 338902 BA
21	235.2	70.6	488	10	BE49441	BE49441 476833 MA
22	235.2	70.6	489	10	BE476453	BE476453 159697 BA
23	235.2	70.6	491	10	BE692788	BE692788 342607 BA
24	234.2	70.3	420	10	BE482648	BE482648 168498 BA
25	233.8	70.2	528	10	BE688615	BE688615 336301 BA
26	233.6	70.2	471	10	BE774840	BE774840 284827 MA
27	232	69.7	517	10	BE483056	BE483056 169073 BA
28	230.4	69.2	557	10	BM088825	BM088825 502373 MA
29	230.2	69.1	413	10	BE478852	BE478852 163292 BA
30	229.2	68.8	363	10	BE231054	BE231054 253265 BA
31	228.6	68.6	417	10	BE688700	BE688700 364148 BA
32	227.2	68.2	508	10	BE481939	BE481939 167555 BA
33	227.2	68.2	623	10	BE692841	BE692841 342685 BA
34	225.6	67.7	541	10	BM087227	BM087227 499922 MA
35	224.2	67.3	396	10	BE482524	BE482524 168348 BA
36	222.8	66.9	586	10	BE688462	BE688462 336092 BA
37	222.6	66.8	562	10	BE48653	BE48653 471154 MA
38	220.8	66.3	513	10	BE483284	BE483284 169398 BA
39	219.8	66.0	458	10	BE484396	BE484396 170935 BA
40	219.2	65.8	508	10	BE481887	BE481887 167492 BA
41	219.2	65.8	549	10	BE691624	BE691624 340869 BA
42	218.8	65.7	386	10	BE692356	BE692356 342021 BA
43	217.6	65.3	465	10	BE478405	BE478405 162646 BA
44	217.6	65.3	518	9	AM462441	AM462441 BE230009A
45	216.2	64.9	476	10	BE690901	BE690901 339802 BA

## ALIGNMENTS

RESULT 1  
BE476752 451 bp mRNA linear EST 28-AUG-2000  
160141 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
BE476752  
BE476752.1 GI:9596285

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414

Email: tadselpsi@ars.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -mismatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTTCCAGTACACAGC  
Plate: 28 row: K column: 18  
Seq primer: ATTTAGGTGACACTAATAG.  
Location/Qualifiers  
1..451

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pcMV SPORTE; Site\_1: XbaI; Site\_2: XhoI;

## FEATURES

## source

BE688590 336269 BA  
BE588329 194153 BA  
BE690381 338902 BA  
BE49441 476833 MA  
BE476453 159697 BA  
BE692788 342607 BA  
BE482648 168498 BA  
BE688615 336301 BA  
BE774840 284827 MA  
BE483056 169073 BA  
BM088825 502373 MA  
BE478852 163292 BA  
BE231054 253265 BA  
BE688700 364148 BA  
BE481939 167555 BA  
BE692841 342685 BA  
BM087227 499922 MA  
BE482524 168348 BA  
BE688462 336092 BA  
BE48653 471154 MA  
BE483284 169398 BA  
BE484396 170935 BA  
BE481887 167492 BA  
BE691624 340869 BA  
BE692356 342021 BA  
BE478405 162646 BA  
AM462441 BE230009A  
BE690901 339802 BA

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 75 a 160 c 123 g 93 t

ORIGIN

Query Match 82.7%; Score 275.4; DB 10; Length 451;  
Best Local Similarity 89.2%; Pred. No. 1.9e-62;  
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 cagagatgtgtcactcagccgtccctcgtctcgtggtcccttgagcagaggtctccatc 60  
|||||  
Db 79 CAGGCTGTGCTGACTCAGCCGCTCCGCTCCGCGGTCCCTGGGCCAGAGGCTCCATC 138  
QY 61 acctgtcttgaagcagcagcaacatttgagtaattgtctatgtggtctgtlaccacag 120  
|||||  
Db 139 ACCTGCTCTGGAAGCAGCAGCAGCTTGGAACCTGGCAATTATGTGACTGTGTTCCAAAC 198  
QY 121 gtcccaagatcagcccccagactcctcatcagtgtctacaacagatcagctcggggatc 180  
|||||  
Db 199 ATCCAGGATCGGCCCCCAACACCTTCATCTATGCTCCGACAGTCAGCCTCGGGGCTC 258  
QY 181 cccgaccgattctccggtctcaggtctcgtggaacacagccacccctgaccatcagctgctc 240  
|||||  
Db 259 CCCGACCGATTCTCCGCTCCAGCTCTGGGAACACGACCCCTGACCATCAGCTCGCTC 318  
QY 241 caggctgaagcagcagcgccgatttactgtgcacgtcgtataaagttactcagttggtt 300  
|||||  
Db 319 CAGGCTGAGCAGCAGGAGATTTATTTCTGTGCATCTTATCAGAGTGTGACACAGCGTGT 378  
QY 301 ttccgacgagcgagcagcgctcagcgtctcgtgt 333  
|||||  
Db 379 TTCCGACGCGGACACGCTGACCGTCTCGGT 411

## RESULT 2

BEA76398 515 bp mRNA linear EST 28-AUG-2000  
LOCUS BEA76398 159628 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BEA76398  
VERSION BEA76398.1 GI:9595931  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 515)  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
AUTHORS gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psl.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 27 row: G column: 1  
Seq primer: ATTTAGGTGACACTATAG.  
Location/Qualifiers  
1. 515

## FEATURES

source  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"

/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPOR6; Site 1: XbaI; Site 2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 98 a 178 c 132 g 107 t

ORIGIN

Query Match 80.8%; Score 269; DB 10; Length 515;  
Best Local Similarity 88.0%; Pred. No. 9.7e-61;  
Matches 293; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 cagagatgtgtcactcagccgtccctcgtctcgtggtcccttgagcagaggtctccatc 60  
|||||  
Db 87 CAGGCTGTGCTGACTCAGCCGCTCCGCTCCGCGGTCCCTGGGCCAGAGGCTCCATC 146  
QY 61 acctgtcttgaagcagcagcaacatttgagtaattgtctatgtggtctgtlaccacag 120  
|||||  
Db 147 ACCTGCTCTGGAAGCAGCAGCAGCTTGGAACCTGGCAATTATGTGACTGTGTTCCAAAC 206  
QY 121 gtcccaagatcagcccccagactcctcatcagtgtctacaacagatcagctcggggatc 180  
|||||  
Db 207 ATCCAGGATCGGCCCCCAACACCTTCATCTATGCTCCGACAGTCAGCCTCGGGGCTC 266  
QY 181 cccgaccgattctccggtctcaggtctcgtggaacacagccacccctgaccatcagctgctc 240  
|||||  
Db 267 CCCGACCGATTCTCCGCTCCAGATCTGGGAACACGACCCCTGACCATCAGCTCGCTC 326  
QY 241 caggctgaagcagcagcgccgatttactgtgcacgtcgtataaagttactcagttggtt 300  
|||||  
Db 327 CAGGCTGAGCAGCAGGAGATTTATTTCTGTGCATCTTATCAGAGTGTGACACAGCGTGT 386  
QY 301 ttccgacgagcgagcagcgctcagcgtctcgtgt 333  
|||||  
Db 387 TTCCGACGCGGACACGCTGACCGTCTCGGT 419

## RESULT 3

BEA85669 495 bp mRNA linear EST 28-AUG-2000  
LOCUS BEA85669 172803 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BEA85669  
VERSION BEA85669.1 GI:9605202  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 495)  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
AUTHORS gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psl.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 132 row: F column: 18  
Seq primer: ATTTAGGTGACACTATAG.  
Location/Qualifiers  
1. 495

## FEATURES

source  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"

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/organism="Bos taurus"  
/db_xref="taxon:9913"  
/clone_lib="BARC 580V"  
/tissue_type="pooled"  
/lab_host="DH10B"  
/note="Vector: PCMV SPOR6; Site_1: XbaI; Site_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT      95 a      174 c      131 g      95 t  
ORIGIN  
  
Query Match      79.8%; Score 265.8; DB 10; Length 495;  
Best Local Similarity 87.4%; Pred. No. 6.7e-60;  
Matches 291; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
  
QY 1 caggatgtctgactcagaccgtctccgtgtctgtgtgtccctggccagaggtctccatc 60  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 87 CAGGCTGTGCTGACTCAGCGGCTCTCGGTCCGGGTCCCTGGCCAGAGGCTCCATC 146  
  
QY 61 acctgtcttggaaagcagcaacattggaagttaattgttctgtgtgtgtaccacag 120  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 147 ACCTGCTCTGGGAAGCAGCAAGAGCTTGAACAGCAATTTGTGAGCTGGGTGCAACAG 206  
  
QY 121 gtccagagatcagcccccagactccatcagtgtgtacaaacagatcgagctcgaggatc 180  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 207 ATCCAGAGATCGGCCCCCAACACCTTCATCTATGCTGCCAGCTCAGGCTCCGGGGTCTC 266  
  
QY 181 cccgaccgattcttcggtctcaggtctgtggaacacagccaccctgacatcagctcgtc 240  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 267 CCCGACCGATTCTCGGCTCCAGGTCTGGGAACAGACCCCTGACCATCAGCTGCTCTC 326  
  
QY 241 caggtctggaagcagagccgatttactgtgcatcgatataaagttacttcaagtgtgt 300  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 327 CAGGCTGAGAGCAGGAGCAGATTATTCTGTGCACTTGTGCAATTTGTATACAAATGCTTT 386  
  
QY 301 ttccgacgagcagcagagctgacgtctcgtgt 333  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 387 TTCGGCAGCGGAGCACACTGACCTGCTGTGGT 419  
  
RESULT 4  
LOCUS BE589073 564 bp mRNA linear EST 28-AUG-2000  
DEFINITION 194817 BARC 580V Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE589073  
VERSION BE589073.1 GI:9842112  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 564)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and  
Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tadelspl.barc.usda.gov  
Single pass sequencing. Bases called and alt.-trimmed with phred  
v0.980904.e. Vector identified by cross_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 121 row: M column: 18
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Seq primer: ATTAGTGACACTATAG.  
Location/Qualifiers  
FEATURES  
source  
1..564  
/organism="Bos taurus"  
/db_xref="taxon:9913"  
/clone_lib="BARC 580V"  
/tissue_type="pooled"  
/lab_host="DH10B"  
/note="Vector: PCMV SPOR6; Site_1: XbaI; Site_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT      106 a      191 c      155 g      112 t  
ORIGIN  
  
Query Match      76.9%; Score 256.2; DB 10; Length 564;  
Best Local Similarity 85.6%; Pred. No. 2.4e-57;  
Matches 285; Conservative 0; Mismatches 48; Indels 0; Gaps 0;  
  
QY 1 caggatgtctgactcagaccgtctccgtgtctgtgtgtccctggccagaggtctccatc 60  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 100 CAGGCTGTGCTGACTCAGCGGCTCTCGGTCCGGGTCCCTGGCCAGAGGATCTCCATC 159  
  
QY 61 acctgtcttggaaagcagcaacattggaagttaattgttctgtgtgtgtaccacag 120  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 160 ACCTGCTCTGGGAAGCAGCAAGAGCTTGAACAGCAATTTGTGAGCTGGTTCACACAG 219  
  
QY 121 gtccagagatcagcccccagactccatcagtgtgtacaaacagatcgagctcgaggatc 180  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 220 ATCCAGAGATCGGCCCCCAACACCTTCATCTATGCTGCCAGCTCAGGCTCCGGGGTCTC 279  
  
QY 181 cccgaccgattcttcggtctcaggtctgtggaacacagccaccctgacatcagctcgtc 240  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 280 CCCGACCGATTCTCGGCTCCAGGTCTGGGAACATFACCACCCCTGACCATCAGCTGCTCTC 339  
  
QY 241 caggtctggaagcagagccgatttactgtgcatcgatataaagttacttcaagtgtgt 300  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 340 CAGGCTGAACACGAGCAGATTATTCTGTGCACTTATTGAGGTGTAGGACAGCTGTT 399  
  
QY 301 ttccgacgagcagcagagctgacgtctcgtgt 333  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 400 TTCGGCAGCGGAGCACTGACCTGCTGTGGT 432  
  
RESULT 5  
LOCUS BG691510 655 bp mRNA linear EST 02-MAY-2001  
DEFINITION 340705 BARC 580V Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BG691510  
VERSION BG691510.1 GI:13933330  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 655)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and  
Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tadelspl.barc.usda.gov  
Single pass sequencing. Bases called and alt.-trimmed with phred  
v0.980904.e. Vector identified by cross_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers
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FORWARD: AGGAAACAGCTATGACCAT  
BACKWARD: GTTTCCCGAGTCACGACG  
Plate: 99 row: 1 column: 6  
Seq primer: ATTAGGTGACACTATAG.  
Location/Qualifiers

## FEATURES

source  
1. 655  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/issue\_type="pooled"  
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 129 a 221 c 181 g 124 t  
ORIGIN

Query Match 75.4%; Score 251.2; DB 10; Length 655;  
Best Local Similarity 86.3%; Pred. No. 5.2e-56;  
Matches 290; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 1 cagagatgctgactcagccgctccctcgtctcgtggtccctcgtgagcgaaggtctccatc 60  
DB 88 CAGAGTGTGCTGACTCAGCCGCTCCTCCGTGCGGGTCCCTGGCCAGAGGGTCTCCATC 147  
QY 61 acctgtcttgaagcagcagcaacatctgagatgtaattgtatgtggctgtacacaag 120  
DB 148 ACCGTGCTGGAGACACACACATGTTGGAATGGCAATTATGTGAGCTGTTCACACAG 207  
QY 121 gtccagagatcagcccccagactccctcatcagtgctacaaacgatacagcctcggggatc 180  
DB 208 ATCCAGAGATCGGCCCCCAAAATGCTCATCTATGATGTCGACACAGTCGAGCCTCGGGGTC 267  
QY 181 ccgagaccattctccggtccaggtcaggtcggagaaacagcccccgtaccatcagctcgtc 240  
DB 268 CCCGACCGATTCTCCGGCTCCAGGTCGAGGAACACACACCCTGACCATCAGCTCCCTC 327  
QY 241 caggctgaagcagcagcgcatattactgtcatcgtatca---aaatcttaccagtggt 297  
DB 328 CAGGCCGAGACGACGCGGATTTATTTCTGTGCATCTCTGACACTATACAGAGAGTTT 387  
QY 298 gtttcgagcagcgagaccaggtcagccgtccctgggt 333  
DB 388 TTTTTCGGCAGCGGACACACACTGACCTGCTGGGT 423

RESULT 6  
BE590205 467 bp mRNA linear EST 28-AUG-2000

LOCUS BE590205  
DEFINITION 197215 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE590205  
VERSION BE590205.1 GI:9843244  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and  
Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Km 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers

FORWARD: AGGAAACAGCTATGACCAT  
BACKWARD: GTTTCCCGAGTCACGACG  
Plate: 117 row: M column: 12  
Seq primer: ATTAGGTGACACTATAG.  
Location/Qualifiers

## FEATURES

source  
1. 467  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 83 a 161 c 126 g 97 t  
ORIGIN

Query Match 75.0%; Score 249.6; DB 10; Length 467;  
Best Local Similarity 86.0%; Pred. No. 1.2e-55;  
Matches 289; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 cagagatgctgactcagccgctccctcgtctcgtggtccctcgtgagcgaaggtctccatc 60  
DB 74 CAGAGTGTGCTGACTCAGCCGCTCCTCCGTGCGGGTCCCTGGCCAGAGGGTCTCCATC 133  
QY 61 acctgtcttgaagcagcagcaacatctgagatgtaattgtatgtggctgtacacaag 120  
DB 134 ACCGTGCTGGAGACACACGCAATATGGAATGGCAATTATGTGAGCTGTTCACACAG 193  
QY 121 gtccagagatcagcccccagactccctcatcagtgctacaaacgatacagcctcggggatc 180  
DB 194 ATCCAGAGATCGGCCCCCAAAATGCTCATCTATGATGTCGACACAGTCGAGCCTCGGGGTC 253  
QY 181 ccgagaccattctccggtccaggtcaggtcggagaaacagcccccgtaccatcagctcgtc 240  
DB 254 CCCGACCGATTCTCCGGCTCCAGGTCGAGGAACACACACCCTGACCATCAGCTCCCTC 313  
QY 241 caggctgaagcagcagcgcatattactgtcatcgtatca---agtgt 297  
DB 314 CAGGCCGAGACGACGCGGATTTATTTCTGTGCATCTCTGACACTATACAGAGAGTGT 373  
QY 298 gtttcgagcagcgagaccaggtcagccgtccctgggt 333  
DB 374 AGATTTCGGCAGCGGACACACACTGACCTGCTGGGT 409

RESULT 7  
BE487574 493 bp mRNA linear EST 28-AUG-2000

LOCUS BE487574  
DEFINITION 176397 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE487574  
VERSION BE487574.1 GI:9607107  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and  
Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Km 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416



Fax: 301 504 8414  
 Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt\_trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
 and -mismatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 138 row: L column: 11  
 Seq primer: ATTTAGTGACACTATAG.

## FEATURES

source

Location/Qualifiers

1..493

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_lib="BARC 5BOV"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT 95 a 173 c 127 g 98 t

ORIGIN

Query Match 74.5%; Score 248.2; DB 10; Length 493;

Best Local Similarity 86.2%; Pred. No. 2.9e-55;

Matches 287; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

QY 1 cagagatgtctgaactcaagcgcctcctcgtgtctgtgtcccttgagcagaggtctccatc 60

DB 89 CAGGCTGTCTGACTCAGCCGCTCCGTCGCGGTCCTCCGCGGCGCAGAGAGCTCTCATC 148

QY 61 acctgtcttgaggaagcagcaacattgaggttaagtctatgtgtgtgtgtgtgtgtgtgt 120

DB 149 ACCCTGCTCTGGAAGCAATCAACGTCGGAACCTGCAATTAATGCTGTGCTGCTCAACAG 208

QY 121 gtccagagatcagccccagactcctcatcagtgctacacagatcagagctcagagatc 180

DB 209 ATCCGAGATCAGCCCCAGAACCCCTCATGTATGTGTGCGACAGCTGACCTCGGGGCTC 268

QY 181 cccagacgatctcgcgctcagagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240

DB 269 CCCGACCGATCTCCGGCTCTAGCGCTGCGGAGAACACACCCCTGACATCAACTCGCTC 328

QY 241 cagagctgaggaagcagcgatatactgtgtcatgtatcaagatcactacagtggtgt 300

DB 329 CAGGCTGAGAGCAGGACGATTAATTTCTGTGATCTTATCAGAGTGT--AAATGCTGT 385

QY 301 ttcgagcagcgagcagagctgacgctcgtgtgt 333

DB 386 TTCGCGAGCGGAGCACACTGACCGCTGTGGGT 418

## RESULT 8

LOCUS BG688999 467 bp mRNA linear EST 02-MAY-2001

DEFINITION BG688999 336848 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BG688999

VERSION BG688999.1 GI:13930800

KEYWORDS EST.

SOURCE EST.

ORGANISM Bos taurus

COW.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 467)

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL Unpublished (2000)

COMMENT Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt\_trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
 and -mismatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 103 row: H column: 3  
 Seq primer: ATTTAGTGACACTATAG.

## FEATURES

source

Location/Qualifiers

1..467

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_lib="BARC 5BOV"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT 85 a 161 c 128 g 93 t

ORIGIN

Query Match 73.1%; Score 243.4; DB 10; Length 467;

Best Local Similarity 85.3%; Pred. No. 5.2e-54;

Matches 284; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 cagagatgtctgaactcaagcgcctcctcgtgtctgtgtcccttgagcagaggtctccatc 60

DB 88 CAGGCTGTCTGACTCAGCCGCTCTCCGTCGCGGTCCTCCGCGGCGCAGAGGCTCTCATC 147

QY 61 acctgtcttgaggaagcagcaacattgaggttaagtctatgtgtgtgtgtgtgtgtgtgt 120

DB 148 ACTGCTCTGGAAGTGAAGCATATCGGTATGATG--GTGTGGGCTGTGTCAACAG 204

QY 121 gtccagagatcagccccagactcctcatcagtgctacacagatcagagctcagagatc 180

DB 205 GTCCGAGATCGGGGCTCCAGAACATCAATCTATGATGATGATGATGATGATGATGATG 264

QY 181 cccagacgatctcgcgctcagagtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240

DB 265 CCCGACCGATCTCCGGCTCTAGCGCTGCGGAGAACACACCCCTGACATCAACTCGCTC 324

QY 241 cagagctgaggaagcagcgatatactgtgtcatgtatcaagatcactacagtggtgt 300

DB 325 CAGGCTGAGAGCAGGCGGATTAATTTCTGTGATCTTATCAGAGTGT--AAATGCTGT 384

QY 301 ttcgagcagcgagcagagctgacgctcgtgtgt 333

DB 385 TTCGCGAGCGGAGCACACTGACCGCTGTGGGT 417

## RESULT 9

LOCUS BE476758 496 bp mRNA linear EST 28-AUG-2000

DEFINITION BE476758 160150 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE476758

VERSION BE476758.1 GI:9596291

KEYWORDS EST.

SOURCE EST.

ORGANISM Bos taurus

COW.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 496)

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL  
COMMENT  
gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tadelpsi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 28 row: L column: 3  
Seq primer: ATTAGGTGACACTATAG.  
Location/Qualifiers  
1. 496  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT  
ORIGIN  
98 a 167 c 133 g 98 t

Query Match  
Best Local Similarity 73.0%; Score 243.2; DB 10; Length 496;  
Matches 292; Conservative 0; Mismatches 38; Indels 6; Gaps 2;

1 caggatgctgctgactagccgctcctcgtgctggttcctcgtgaggggtctcctc 60  
|||||  
89 CAGGCTGTGTGATCAGCATATCAGTGTCCGGTCCCTGGGCGAGAGGCTCTCATC 148  
|||||  
61 acctgctctggaagcagcagcaacattggaagtaattgcttatgtggctctgtac 120  
|||||  
149 ACTGCTCTGGAGACGACGACATGTTGGA---AATGATATGTAGCTGTACCAACTG 205  
|||||  
121 gtccagagatcagcccccagactccctcattcagtgtacaaacagatcgagcctc 180  
|||||  
206 ATCCAGAGATCGGCGCCCAACCTCATCTATGTGTGACACACAGTCCGCGG 265  
|||||  
181 cccgacgattctcgcgtcccaagctctggaacacagcaccctgaccatcaactgc 240  
|||||  
266 CCCGACCGATTCTCCGGCTCCAGGCTCTGGGAACACAGCCCTGACACATCACTG 325  
|||||  
241 caggctgaggaagcagcagattactgtgcatcgatcaaaagtactactacag---t 297  
|||||  
326 CAGGCTGAGAGACGAGCAGATTATTTCTGTGCACTGTGCTAGAGATAGTACATA 385  
|||||  
298 gttttcgagcagcagcagcagctgacctgtggt 333  
|||||  
386 GTTTTCGGCAGCGGACACACTGACACTGCTGGGT 421  
|||||

RESULT 10  
LOCUS BG689524 484 bp mRNA linear EST 02-MAY-2001  
DEFINITION 337633 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BG689524  
VERSION BG689524.1 GI:13931325  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 484)

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and  
Wells, K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tadelpsi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACAGTCACGACG  
Plate: 102 row: K column: 2  
Seq primer: ATTAGGTGACACTATAG.  
Location/Qualifiers  
1. 484  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT  
ORIGIN  
86 a 161 c 136 g 101 t

Query Match  
Best Local Similarity 72.1%; Score 240.2; DB 10; Length 484;  
Matches 275; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

1 caggatgctgctgactagccgctcctcgtgctggttcctcgtgaggggtctcctc 60  
|||||  
93 CAGGCTGTACTGATCAGCGGCTCTCCGTGTCGGGTCCCTGGGCGAGAGGCTCTCATC 152  
|||||  
61 acctgctctggaagcagcagcaacattggaagtaattgcttatgtggctctgtac 120  
|||||  
153 ACTGCTCTGGAGACGACGACATGTTGCACTTGCCAAATGATGTGATTGTTCCAAAG 212  
|||||  
121 gtccagagatcagcccccagactccctcattcagtgtacaaacagatcgagcctc 180  
|||||  
213 ATCCAGAGATCGGCGCCCAAAATGTCATCTATGTGTGCGACGACGACACCTCTGGG 272  
|||||  
181 cccgacgattctcgcgtcccaagctctggaacacagcaccctgaccatcaactgc 240  
|||||  
273 CCCGACCGATTCTCCGGCTCCAGGCTCTGGGAACACAGCCCTGACACATCACTG 332  
|||||  
241 caggctgaggaagcagcagattactgtgcatcgatcaaaagtactactacagtggt 300  
|||||  
333 CAGGCCGAGAGACGAGCGGCTATTATTTGTCTTCCTGTGATAGTACGCTGTGATT 392  
|||||  
301 ttccgagcagcagcagcagcagctgacctgtggt 333  
|||||  
393 TTCCGCGCGCGGACCACTAAGCTGTGGGT 425  
|||||

RESULT 11  
LOCUS BE483566 518 bp mRNA linear EST 28-AUG-2000  
DEFINITION 169766 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE483566  
VERSION BE483566.1 GI:9603099  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 518)  
Sontegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and  
Wells, K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
Unpublished (2000)  
Contact: Sontegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tad@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt. trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTGACGACGACG  
Plate: 23 row: L column: 14  
Seq primer: ATTAGCTGACACTATAG.  
Location/Qualifiers  
1. 518  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 580V"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 101 a 177 c 141 g 99 t

ORIGIN

Query Match 72.1%; Score 240; DB 10; Length 518;  
Best Local Similarity 86.3%; Pred. No. 4.3e-53;  
Matches 290; Conservative 0; Mismatches 40; Indels 6; Gaps 2;

QY 1 caggatgtgtctgactcagcgcgtctcgtgtctgtgtccctgtgagccagaggtctccatc 60  
DB 92 CAGGCTGTGCTGACTGACTGACCATCATCGTGTCCGGGCTCCCTGGGCGAGGGTCTCCATC 151  
QY 61 acctgtcttggaaagcagcagcaacattggaggttaagtctatgttggtctgttaccacag 120  
DB 152 ACCTGACCGGAGAGCAGCAATGTTGA--AATGGATATGTGACCTGTTCCAAACAG 208  
QY 121 gtcccaagatcagcccccagactccatcagtgctgtacacacgactcagcctcgggagtc 180  
DB 209 ATCCAGAGATCGGCCCCCAGAACCTTCATCTATGTGACACAGTCCAGGCTGGGGGTC 268  
QY 181 cccgaccgattctcgcgtctcaggtctgtggaacacagccaccctgacatcagctcgtc 240  
DB 269 CCCGACCGATTCTCCGGCTCCAGGTCTGGGAGACACGCCCTGACCATCAGCTCGCTC 328  
QY 241 caggctgagagcagagccgattatctactgtgcatcgatataaagtacttcag--tggt 297  
DB 329 CAGGCTGAGATGAGCGAGATTATTTCTGTGAGCTGTGACAGAGTACAGATTAATGCT 388  
QY 298 gtttcgagcgggagccagcgtcagcgtctcgtgt 333  
DB 389 GTTTTCGGCAGCGGACACACTGACCGCTCGGGT 424

RESULT 12  
LOCUS BE751028 542 bp mRNA linear EST 25-APR-2001  
DEFINITION 202731 MARC 280V Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE751028  
VERSION BE751028.1 GI:10165020  
KEYWORDS EST.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

cow.  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 542)  
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Casas, E., Wray, J.E., Laegreid, W.W., Rohrer, G.A., Chitko, McKown, C.G.,  
Petrica, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and  
Keeler, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)  
21180013  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt. trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTGACGACGACG  
Plate: 42 row: B column: 15  
Seq primer: ATTAGCTGACACTATAG.  
Location/Qualifiers  
1. 542  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 280V"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from testis, thymus,  
semilandonous muscle, longissimus muscle, pancreas,  
adrenal, and endometrium."

BASE COUNT 102 a 183 c 144 g 112 t 1 others

ORIGIN

Query Match 71.9%; Score 239.4; DB 10; Length 542;  
Best Local Similarity 86.2%; Pred. No. 6.3e-53;  
Matches 288; Conservative 0; Mismatches 42; Indels 4; Gaps 2;

QY 1 caggatgtgtctgactcagcgcgtctcgtgtctgtgtccctgtgagccagaggtctccatc 60  
DB 92 CAGGCTGTGCTGACTGACTGACCGCTCTCCGTGTCCGGCTCCCTGGGCGAGGGTCTCCATC 151  
QY 61 acctgtcttggaaagcagcagcaacattggaggttaagtctatgttggtctgttaccacag 120  
DB 152 ACCGCTCTGGAAGACACACAACAT--CGGTGATATGATGAGGCTGTACCAACAG 208  
QY 121 gtcccaagatcagcccccagactccatcagtgctgtacacacgactcagcctcgggagtc 180  
DB 209 GTCCACGATCGGCGCTCATTAACCATCATCTATGTGTGACACTGACCTCGGGGTC 268  
QY 181 cccgaccgattctcgcgtctcaggtctgtggaacacagccaccctgacatcagctcgtc 240  
DB 269 CCCGACCGATTCTCCGGCTCCAGTCTGGGAGACACAGCCCTGACCATCAGCTCGCTC 328  
QY 241 caggctgagagcagagccgattatctactgtgcatcgatataaagtacttcagt-99tgt 299  
DB 329 CAGGCTGAGATGAGCGCGAGATTATTTCTGTGACTATGACAGTACTAGACGATTAATGCT 388  
QY 300 ttctcgagcgggagccagcgtcagcgtctcgtgt 333  
DB 389 TTTTCGGCAGCGGACACATTGACCGCTCGGGT 422

RESULT 13  
BE722165 557 bp mRNA linear EST 25-APR-2001  
LOCUS 190280 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION BE722165  
ACCESSION BE722165  
VERSION BE722165.1 GI:10123461  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 557)  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Peters,G., Holt,I., Karayancheva,S., Liang,F., Quackenbush,J. and  
Keeler,J.W.  
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4396  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 102 row: L column: 3  
Seq primer: ATTAGTGACTATAG.  
Location/Qualifiers  
1..557  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 4BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from day 20 and day 40  
embryos."

BASE COUNT 115 a 175 c 142 g 125 t  
ORIGIN  
Query Match 71.4%; Score 237.6; DB 10; Length 557;  
Best Local Similarity 88.4%; Pred. No. 1.9e-52;  
Matches 258; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 1 caggatgtgtgactacgcgctctccggtctcgtgtcgtggtccctggcgcaagaggtctcatc 60  
DB 89 CAGGCTGTGCTGACTCAGCGCTCCTCGTGTCCGGGTCCTGGGCGCAGAGGCTCTCCATC 148  
QY 61 acctgctctggaacgaacgaacattggaagttaattgtatgtggtggtgttaccacag 120  
DB 149 ACCTGCTCTGGAACGACGACGACGATTGATATGGCAATTATGTGAGCTGGTTCACAG 208  
QY 121 gtccagagatcagcccccaactcctcatcagtgtagtacaacagatcgagctcgagatc 180  
DB 209 ATCCAGAGATCGGGCCACAGACCTCATATGATGTGACACACATGACGCTCGGGGCTC 268  
QY 181 ccgagaccgattctcgggtccaggtctgtggaacacagcacacctgaccatcagctgc 240  
DB 269 CCCGACCGATTCTCCGGCTCCAGGCTGTGGGAACACAGCCCTGACCATCAGCTCCGCTC 328  
QY 241 caggctagagagagcgagcttactgtgcatcgatataagtlacttaca 292  
DB 329 CAGGCTGAGGACGAGGAGATTATTCTGTGCACTTATCAGAGTGGTAAACA 380

RESULT 14  
BE485929 503 bp mRNA linear EST 28-AUG-2000  
LOCUS 173232 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION BE485929  
ACCESSION BE485929  
VERSION BE485929.1 GI:9605462  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 503)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,L.C.P., Ashwell,M.S. and  
Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@aps1.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 131 row: H column: 15  
Seq primer: ATTAGTGACTATAG.  
Location/Qualifiers  
1..503  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 92 a 175 c 134 g 102 t  
ORIGIN  
Query Match 71.1%; Score 236.8; DB 10; Length 503;  
Best Local Similarity 85.7%; Pred. No. 3e-52;  
Matches 288; Conservative 0; Mismatches 42; Indels 6; Gaps 2;  
QY 1 caggatgtgtgactacgcgctctccggtctcgtgtcgtggtccctggcgcaagaggtctcatc 60  
DB 89 CAGGCTGTGCTGACTCAGCGCTCCTCGTGTCCGGGTCCTGGGCGCAGAGGCTCTCCATC 148  
QY 61 acctgctctggaacgaacgaacattggaagttaattgtatgtggtggtgttaccacag 120  
DB 149 ACCTGCTCTGGAACGACGACGACGATTGATATGGCAATTATGTGAGCTGGTTCACAG 205  
QY 121 gtccagagatcagcccccaactcctcatcagtgtagtacaacagatcgagctcgagatc 180  
DB 206 GTCCAGAGATCGGGCCACAGACCATCATATGATGTGAGCACTGACGCTCGGGGCTC 265  
QY 181 ccgagaccgattctcgggtccaggtctgtggaacacagcacacctgaccatcagctgc 240  
DB 266 CCCGACCGATTCTCCGGCTCCAGGCTGTGGGAACACAGCCCTGACCATCAGCTCCGCTC 325  
QY 241 caggctagagagagcgagcttactgtgcatcgatataagtlacttaca 297  
DB 326 CAGGCTGAGGACGAGGAGATTATTCTGTGCACTTATCAGAGTGGTAAACA 385



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 22:10:19 ; Search time 376.54 Seconds  
(without alignments)  
1518.385 Million cell updates/sec

Title: US-09-786-015-3

Perfect score: 333  
Sequence: 1 cagatgctgctgactcagcc.....ccagctgacgcctcgtggt 333

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_032802:\*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
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- 18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	333	21	AAA08401
2	206.2	61.9	331	22	AA168771
3	198.4	59.6	935	22	AAC6525
4	197	59.2	339	22	AAH47733
5	195.4	58.7	385	22	AA158663
6	193.6	58.1	738	21	AA255614
7	193.2	58.0	348	22	AAH74666
8	193.2	58.0	915	22	AAH74670
9	193.2	58.0	915	22	AAH74679

10	193	58.0	330	22	AA503520
11	192.2	57.7	628	14	AA036134
12	192.2	57.7	891	22	AAC66528
13	192.2	57.7	1044	12	AAQ12840
14	190.2	57.1	464	22	AAE92354
15	189.6	56.9	333	22	AAH42401
16	189.6	56.9	333	22	AAH42407
17	189.6	56.9	351	22	AA168765
18	189	56.8	330	21	AAA27661
19	189	56.8	482	21	AAC98409
20	188.2	56.5	380	22	AA503477
21	187.4	56.3	390	19	AAV33307
22	187.4	56.3	747	21	AAC67868
23	187.4	56.3	889	23	AA577073
24	187.4	56.3	9071	13	AAQ22491
25	187.4	56.3	9071	13	AAQ23370
26	187.2	56.2	393	18	AAH80759
27	187.2	56.2	933	20	AAV72534
28	186.4	56.0	351	22	AA168755
29	185.8	55.8	333	17	AAH10327
30	185.8	55.8	333	20	AA231655
31	185.8	55.8	756	23	AA583477
32	185.8	55.8	866	23	AA587037
33	185.6	55.7	393	18	AAH72648
34	185.6	55.7	774	18	AAH50787
35	184.2	55.3	333	20	AA231654
36	184	55.3	336	21	AA596953
37	184	55.3	342	24	ABA94217
38	184	55.3	884	11	AAQ03609
39	182.8	54.9	333	20	AAV72226
40	182.4	54.8	334	22	AAH47514
41	182.4	54.8	342	24	ABA94244
42	182.2	54.7	330	11	AAQ03607
43	182	54.7	330	22	AAH68677
44	182	54.7	732	20	AAH86940
45	182	54.7	732	20	AAH86941

#### ALIGNMENTS

RESULT 1  
AAA08401  
ID AAA08401 standard; DNA; 333 BP.  
XX  
AC AAA08401;  
XX  
XX  
DF 13-JUL-2000 (first entry)  
XX  
XX  
DE Carcinoembryonic antigen affinity antibody light chain variable region.  
XX  
XX  
KM Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;  
KW tumour associated antigen; anti-carcinogenic; cytostatic;  
KM cancer therapy; ds.  
XX  
XX  
OS Ovis sp.  
XX  
XX  
PN WO200012556-A1.  
XX  
XX  
PD 09-MAR-2000.  
XX  
XX  
PF 20-AUG-1999; 99WO-CB02729.  
XX  
XX  
PR 28-AUG-1998; 98GB-0018915.  
XX  
XX  
PA (KSBI-) KS BIOMEDIX LTD.  
XX  
XX  
PI Harrison PJ;  
XX  
XX  
DR WPI: 2000-375618/32.  
XX  
XX  
XX P-PSDB: AAH82529.  
XX  
XX  
XX A new high-affinity monoclonal antibody that is characterized by an

PT	acid-washed enzyme-linked immunosorbent assay for use in cancer therapy	
PS	Claim 9; Page 15; 21pp; English.	
XX		
CC	The present invention describes a high-affinity monoclonal antibody	
CC	characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).	
CC	The antibody is used in cancer therapy. Association of the new antibody	
CC	with an antigen is favoured over dissociation in vivo and they therefore	
CC	have longer localisation times at target sites, resulting in a higher	
CC	concentration of antibodies localised at the target sites. Targeting the	
CC	antibody to a site in vivo is improved. The concentration of antibody	
CC	does not need to be too high which reduces side-effects and costs of	
CC	therapy. The present sequence encodes the light chain variable region	
CC	of a monoclonal antibody having affinity for carcinoembryonic antigen	
CC	(CEA, a tumour associated antigen), which is used in the exemplification	
CC	of the present invention.	
XX		
SO	Sequence 333 BP; 66 A; 103 C; 94 G; 70 T; 0 other;	
	Query Match	100.0%; Score 333; DB 21; Length 333;
	Best Local Similarity	100.0%; Pred. No. 2.9e-86;
	Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 caggatgtgctgactcagccgctccgtgctggtggtccctggcgcaaggtctccatc 60	
DB	1 caggatgtgctgactcagccgctccgtgctggtggtccctggcgcaaggtctccatc 60	
QY	61 accgtccttgtaagcaagcaaatgtggaggtgaatgtctatrtgggtctgtatccaacag 120	
DB	61 accgtccttgtaagcaagcaaatgtggaggtgaatgtctatrtgggtctgtatccaacag 120	
QY	121 gtcccaagatcagcccccagactctctatcagtgtctacaacagcatgagctctggggatc 180	
DB	121 gtcccaagatcagcccccagactctctatcagtgtctacaacagcatgagctctggggatc 180	
QY	181 ccgacacgattctccgctcaggtctcgtggaaacagacacccctggaccatcagctcgctc 240	
DB	181 ccgacacgattctccgctcaggtctcgtggaaacagacacccctggaccatcagctcgctc 240	
QY	241 caggctgagagcagagccgcatattactgtgcatcgtatcaaaagtaactaacgtgtgt 300	
DB	241 caggctgagagcagagccgcatattactgtgcatcgtatcaaaagtaactaacgtgtgt 300	
QY	301 ttggcagcgaggacagagctgaccgctcgtgt 333	
DB	301 ttggcagcgaggacagagctgaccgctcgtgt 333	
RESULT	2	
AAI68771		
ID	AAI68771 standard; DNA; 331 BP.	
XX		
CC	AAI68771;	
DT	22-JAN-2002 (first entry)	
XX		
DE	Human autoantibody MICA-10 variable region heavy chain DNA.	
XX		
KW	Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;	
KW	glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;	
KW	polyglutular autoimmune syndrome; autoimmune disorder; RA2; GAD65;	
KW	variable region; heavy chain; MICA-10; ds.	
OS	Homo sapiens.	
XX		
PN	EP1149914-A2.	
XX		
PD	31-OCT-2001.	
XX		
PF	29-MAR-2001; 2001EP-0107702.	
XX		
XX	10-APR-2000; 2000DE-1017782.	
RR		

PR 25-MAY-2000; 2000DE-1025840.  
 XX  
 PA (LABO-) LABOR KOCH MERK GMBH.  
 XX  
 PL Richter W, Rickert M, Rapp I, Dangel W;  
 XX  
 DR WPI, 2001-640702/74.  
 DR P-PSDB; AAG80222.  
 XX  
 PT New fusion protein, useful for diagnosis of diabetes type I and other  
 PT metabolic diseases, is reactive with autoantibodies against both  
 PT glutamate decarboxylase and islet cell antigen -  
 PS  
 PS Disclosure; Page 40-41; 68pp; German.  
 XX  
 XX This invention describes a novel fusion protein (I) that has, at its  
 CC C-terminus, one or more epitopes that bind specifically to autoantibodies  
 CC (Ab) against the islet cell antigen IA2 and, at its C-terminus, one or  
 CC more epitopes that bind specifically to antibodies (Ab) directed against  
 CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding  
 CC it, vectors containing (II) and transformed cells, are useful for  
 CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,  
 CC polyglandular autoimmune syndrome or other autoimmune conditions  
 CC associated with AAB against GAD65 or IA2. (I) provides a rapid and simple  
 CC diagnosis of high specificity and sensitivity, capable of recognizing  
 CC antibodies against both IA2 and GAD65, simultaneously. Unlike known  
 CC fusions, where the GAD65 component is at the N-terminus, (I) contains  
 CC correctly folded conformational epitopes that can react with most MICA  
 CC autoantibodies. This sequence encodes the human autoantibody MICA-10  
 CC variable region heavy chain used in the method of the invention.  
 XX  
 XX Sequence 331 BP; 66 A; 106 C; 91 G; 68 T; 0 other;  
 SO

Query Match	Similarity	61.9%	Score	206.2	DB	22	Length	331
Best Local	Similarity	76.4%	Pred.	No. 8.8e-50				
Matches	253	Conservative	0	Mismatches	78	Indels	0	Gaps
QY	1	caggatgtgctgtactcaacgcgtctctcgtgtctgtctggtcccttggccagaggtctccatc	60					
DB	1		60					
QY	61	acctgtctgtgaagcagcagcaacattggaagtaattgcttatgtgtggtgtgtaccacag	120					
DB	61		120					
QY	121	gtccagagatcagccccagactctctcatgtgttaacaacgatacgagcctccgggatac	180					
DB	121		180					
QY	181	cccgacgcatcttcctcggtctcaggtctgtggaacaacagccacccttaccatacgtccgc	240					
DB	181		240					
QY	241	caggtcttgagcagcaggtccgcatattactgttgcatactgtatacaagtaactacagttgtgt	300					
DB	241		300					
QY	301	ttcggcagcgggaccagcgtgacgctcctggtg	331					
DB	301		331					
RESULT	3							
ID	AAC66525	standard; cDNA; 935 BP.						
XX	AAC66525;							
XX	15-FEB-2001	(first entry)						
XX	Human immune system associated protein HISAP-7 coding sequence.							





AA158663  
 ID AA158663 standard; cDNA; 585 BP.  
 XX  
 AC AA158663;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 866.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukemia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000MO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 XX  
 PT P-PSDB; AAM39507.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Claim 1; SEQ ID NO 866; 10078pp; English.  
 XX  
 XX The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokine activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 CC  
 XX Sequence 585 BP; 113 A; 194 C; 156 G; 122 T; 0 other;  
 SQ

Query Match 58.7%; Score 195.4; DB 22; Length 585;  
 Best Local Similarity 75.8%; Pred. No. 1.3e-46;  
 Matches 257; Conservative 0; Mismatches 76; Indels 6; Gaps 1;  
 QY 1 cagatgtgtctgactcgcgcgtctcgtctgtctgtctgtcctcgtgcagaggtcttcac 60  
 III IIIIIIIII IIIII IIIIIIIII III IIIIIIIII IIIII

DB 124 cagtlctgtctgacgcagccgcctcagtlgtctgtggccccagggcagaggtcaccatc 183  
 QY 61 accgtctctggaagcagcagcagcatgtgaggtgaatgtatgtggtctgtaccacag 120  
 DB 184 tctctgcacttggaagcagcagcagcagcaggtgaggtgaggtgaggtgaggtgaggt 243  
 QY 121 gtccagagatcagcccccagcagcagcagcagcagcagcagcagcagcagcagcagcag 180  
 DB 244 cttccaggaacagcccccagcagcagcagcagcagcagcagcagcagcagcagcagcag 303  
 QY 181 ccgagcagatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 240  
 DB 304 cctgagcagatctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 363  
 QY 241 cagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 297  
 DB 364 cagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 423  
 QY 298 ---gttctcgacgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 333  
 DB 424 gtgtatctcgcgagggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 462

RESULT 6  
 AA255614  
 ID AA255614 standard; cDNA; 738 BP.  
 XX  
 AC AA255614;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Internalising anti-c-erbB-2 receptor antibody scFv F5 cDNA.  
 KW Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;  
 KW HBR/neu oncogene; tumour-specific; internalisation; non-immunogenic; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT mat\_peptide 1..738  
 FT /\*tag= a  
 FT /product= "Internalising anti-c-erbB-2 antibody F5"  
 XX  
 PN WO955367-A1.  
 XX  
 PD 04-NOV-1999.  
 XX  
 PF 23-APR-1999; 99WO-US07395.  
 XX  
 PR 24-APR-1998; 98US-0082953.  
 PR 12-FEB-1999; 99US-0250056.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Marks JD, Poul MA;  
 XX  
 DR WPI; 2000-072168/06.  
 DR P-PSDB; AAY58235.  
 XX  
 PT Novel internalizing antibodies used to treat cancer cells -  
 XX  
 PS Claim 45; Page 81; 85pp; English.  
 XX

This sequence represents cDNA encoding an internalising humanised  
 CC antibody, scFv F5, which specifically binds to the extracellular domain  
 CC of the c-erbB-2 receptor, the protein product of the HBR/neu oncogene.  
 CC The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that  
 CC is bound by F5 antibodies. On binding the c-erbB-2 receptor, the  
 CC antibody is transported into the cell. The c-erbB-2 receptor is a marker  
 CC protein which is overexpressed by 30-50% of breast carcinomas and other  
 CC adenocarcinomas, and thus provides a useful cell surface marker for  
 CC specifically targeting tumour cells. The antibodies of the invention

are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin; radionuclides; ligands such as growth factors; therapeutic agents such as vinblastine, vindesine or melphalan; ribozymes; or antisense molecules. The antibodies may also be used in vivo or in vitro for detection and/or quantitation of the c-erb-2 receptor and thus diagnosis and/or localisation of cancers characterised by expression of c-erb-2. Although antibodies have previously been used to target tumour cells, their success has been limited. The utility of prior art antibodies has been hampered by the paucity of tumour specific antibodies, antibody immunogenicity, low binding affinity, and poor tumour penetration. Immunogenicity could be avoided and toxicity reduced if high affinity tumour specific human antibodies were available. However, the production of human monoclonal antibodies using conventional hybridoma technology has proven difficult. Also, most of the antibodies produced react with antigens that are also common to non-malignant cells, which makes them unsuitable for use as tumour-targeting molecules. The antibodies of the invention overcome these difficulties, as they are targeted to a tumour-specific antigen, and avoid the problem of immunogenicity as they are human in origin.

Sequence 738 BP; 145 A; 204 C; 232 G; 157 T; 0 other;

Query Match 58.1%; Score 193.6; DB 21; Length 738;

Matches	254;	Conservative	0;	Mismatches	79;	Indels	3;	Gaps	1;
---------	------	--------------	----	------------	-----	--------	----	------	----

[illegible]

RESULT	7
AAH74666	
ID	AAH74666 standard; DNA; 348 BP.

AC AAH74666;

DT 29-OCT-2001 (first entry)

DE Nucleotide sequence of the L chain variable region of SCFV1-4.

KM Complementarity determining region; CDR; single chain antibody; SCFv;  
KM hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;  
KM envelope glycoprotein; ss.

OS Homo sapiens.

PN WO200158459-A1.

PD 16-AUG-2001.

XX 13-FEB-2001; 2001WO-JP00967.  
PF

PR 14-FEB-2000; 2000JP-0034906.

PA (MITS-) MITSUBISHI-TOKYO PHARM INC.

PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

DR WPI; 2001-496986/54.

DR P-PSDB; AAG63630.

PT compounds, by inhibiting binding of hepatitis C virus envelope proteins, sulfated polysaccharides and low-molecular e.g. antibodies, containing substances with antiviral effects for hepatitis C

PS Claim 40; Page 82-83; 138pp; Japanese.

CC The present sequence encodes the L chain variable region of a single  
CC chain antibody of the invention. The specification describes a substance  
CC can inhibit the binding between hepatitis C virus (HCV) and cells with  
CC potential HCV infection, cells with expression of CD81, or CD81. This  
CC substance is especially an antibody with affinity towards HCV E2/NS1  
CC protein, containing amino acid sequences based on the complementarity  
CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable  
CC regions. The antibody inhibits the viral envelope glycoprotein. It is  
CC also a CCR1 inhibitor. The antibodies and drugs are used for treatment  
CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C.

Sequence 348 BP; 72 A; 109 C; 97 G; 70 T; 0 other;

Query Match	58.08;	Score 193.2;	DB 22;	Length 348;
-------------	--------	--------------	--------	-------------

Matches 240; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy	1	cagaatgctgcgcgactcaagccgctccctcgctgtcttggtgctcccttggtccgaagaggtccatc	60
Db	1	cagctctctgctccactcaacccgctccctcctcctgtctctgtgtggtccccaaggtcgaaggtccacatc	60
Qy	61	acctgtctctgaaagcaagcagacgaacatctggaagttaatgtcttaatctggtctgtatccacaag	120
Db	61	tcctctactctggaagcagctccacatccaggtcggtctatgtatgtatgaacctgtatccacag	120
Qy	121	gtcccaagatacgaagccccaagctctcatcaagtcgtctcaacagatcgaatcctgtgggac	180
Db	121	ctcccaagaaacagcccccaacccctccatctatctatgaagtaacaacatcgcctccatgaaggtc	180
Qy	181	cccgaccgaattctcccggtctccaaagtctctgggaacacagccaccctgacacatctgcctc	240
Db	181	ctgtaccgaattctctgtgtctcgaagtctctgcacccctcagccctccgtgcacatcatgtgctc	240
Qy	241	cagagcttgagacacagggcccgatattactctgtgcattcgatataaagaatctcaatctgtgt	300
Db	241	cagagcttgagaggtctgtgctgattatctactctgcagctccatctacacagccctgaatgtgtt	300
Qy	301	ttcggcagcgggaccaga	318
Db	301	gaggtcttcgcgaaccgg	318

RESULT	8
AAH74670	
ID	AAH74670 standard; DNA; 915 BP.

... АС ААН74670;

DT 29-OCT-2001 (first entry)

DE Nucleotide sequence of single chain antibody SCFV1-4.

KW Complementarity determining region; CDR; single chain antibody; ScFv;



```
QY 241 caggctgagagcagcgcattactgtcgtatcgaagctactacgtgtgtt 300
DB 736 caggctgagagatgagcgtctacttactcagctcctatgacagcctgagtgtt 795
QY 301 ttcgcagcgggagcagg 318
DB 796 gagctcttcggaaccgg 813

RESULT 10
AAS03520
ID AAS03520 standard; cDNA: 330 BP.
XX
AC AAS03520;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 106.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW heart disease; complementarity determining region; CDR; ss.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
XX
P-PSDB: AAU02620.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS Disclosure: Page 167; 182pp; English.
XX
CC AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy
CC and light chain coding sequences of the invention. The antibodies can be
CC used in the treatment of obesity and obesity related diseases. The
CC antibodies can be used to deliver drugs or pro-drugs directly to the fat
CC mass of an obese patient or the antibody can be used as a therapeutic
CC itself. Antibodies binding specifically to adipocytes can be used to
CC activate the immune system to destroy the cells by complement mediated
CC lysis. The antibodies may be labeled with a detectable label such as
CC radiolabel, fluorescent or chemical group and used in methods of
CC diagnosis in human subjects e.g. to determine the presence of adipocyte
CC antigen on the surface of an adipocyte to detect or determine the
CC presence or level of adipocytes in a cell or tissue sample. The
CC antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.
XX
SQ Sequence 330 BP; 69 A; 101 C; 83 G; 77 T; 0 other;
```

```
Query Match 58.0%; Score 193; DB 22; Length 330;
Best Local Similarity 74.2%; Pred. No. 5, 5e-46;
Matches 244; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
```

```
QY 1 caggatgtcgtacacgcgtctcgtgtcgtggtccctggcagagggtctccatc 60
DB 1 cagtcgtgtcgtacacgcgtctcgtgtcgtggtccctggcagagggtctccatc 60
```

```
QY 61 acctgtcttggaaagcagcacaacattgaggtatgtctatgtgtggtgtaccacag 120
DB 61 tctgtaccttggaaagcagcacaacattgaggtatgtctatgtgtggtgtaccacag 120
QY 121 gtcccaagatcacgcccccaagctccatcagtgtcgtacacccgatacagctcgaggatc 180
DB 121 caccacaggaagcccccaagctccatcagtgtcgtacacccgatacagctcgaggatc 180
QY 181 cccgaccgattctcgcgtccaggtctggaacacagccaccctgaccatcagctgcctc 240
DB 181 cctgacgtctctcgtctcgaagctcgtgcaacacagctccctgaccgtctcgaagctc 240
QY 241 caggctgagagcagcgcattactactgtcgtatcgaagctactacagtggtgtt 300
DB 241 caggctgagagatgagcgtctacttactgtcaggtcatalatgacgacagcagcagtggtt 300
QY 301 ttcgcagcgggacccagcgtcagctcct 329
DB 301 ttcgcgagggagacccaagctgaccgtcct 329
```

```
RESULT 11
AAQ36134
ID AAQ36134 standard; DNA: 628 BP.
XX
AC AAQ36134;
XX
DT 25-MAY-1993 (first entry)
XX
DE MH4H7 MAb light chain coding sequence.
XX
KW Human; light chain; recombinant; monoclonal; antibody; MAb; MH4H7;
KW Nematelwa; microbial infection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 105..610
FT /*tag= a
FT exon 105..152
FT /*tag= b
FT exon /number= Exon 1
FT Intron 153..266
FT /*tag= c
FT /*number= Intron 1
FT exon 267..610
FT /*tag= d
FT /*number= Exon 2
XX
PN JP04360696-A.
XX
PD 14-DEC-1992.
XX
PF 06-JUN-1991; 91JP-0163886.
XX
PR 06-JUN-1991; 91JP-0163886.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
PA (SUMO ) SUMITOMO SEIYAKU KK.
XX
DR WPI: 1993-032623/04.
XX
P-PSDB: AAR31535.
XX
DR
XX
PT Recombinant human antibody - produced using new human B
PT lymphocyte strain as the host
XX
PS Claim 5; Fig 9; 27pp; Japanese.
XX
CC This sequence encodes the light chain of a recombinant human
CC monoclonal antibody (MAb) designated MH4H7. This sequence was
CC introduced in to a Nematelwa cell strain which was cultured. The
CC MAb may be used in a drug for the prevention and treatment of
```

CC diseases caused by microbial infection.

XX Sequence 628 BP; 109 A; 202 C; 170 G; 147 T; 0 other;

Query Match 57.7%; Score 192.2; DB 14; Length 628;  
Best Local Similarity 73.6%; Pred. No. 1.1e-45;  
Matches 245; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 cagagatgtgtgactcagccgctccgtgtctgtggtccctggccagaggtctccatc 60  
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 278 cagctcgtccgtgactcagctcgtcgtctgtctgtctgtctgtcgtcgtcgtcgtc 337  
QY 61 acctgtcttgaagcagcagcaacatttgaggttaattgttattgttggctgtaccacag 120  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 338 tctgtacttgaacacagcagtgacatgtgtgtatataactatgtctctcgttaccacaa 397  
QY 121 gtcccgagatcagcccccagctccatcattagtggtataacacagatcgagctcggggatc 180  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 398 caccacagcaaacgccccaaactcgtatattatgtctgtcagtaactcggccctcagggtt 457  
QY 181 cccgacagatctcgcgtccagctcaggtctggtggaacacagcacccctgaccatcagctc 240  
| | | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 458 tctcatcgtctctcgtcgtcctcaagctcgtgcaacacggtccctcgtaccatctcgtggtc 517  
QY 241 caggtctgagagcagcagcagatttactgtgcacgtatataaagttacttaagttgtgtt 300  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 518 caggtctgagagcagcagcagtttacttactgcaactcagatgcagcagcagcaaatgtgtt 577  
QY 301 ttccgacgagcagcagcagcgtcgtcgtgtgt 333  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 578 ttccgagagagcagcagcgtcgtcgtgtgt 610

## RESULT 12

AAC6528

ID AAC6528 standard; cDNA; 891 BP.

AC AAC6528;

DT 15-FEB-2001 (first entry)

XX Human immune system associated protein HISAP-10 coding sequence.

XX Human; immune system associated protein; HISAP-10; immune disorder;

KW infection; autoimmune disease; cancer; ss.

XX Homo sapiens.

PN US6135941-A.

PD 24-OCT-2000.

PF 27-MAR-1998; 98US-0049672.

PR 27-MAR-1998; 98US-0049672.

PA (INCYT-) INCYTE PHARM INC.

PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;

PI Hillman JL, Au-Young J;

DR WPI; 2001-030926/04.

DR P-PDB; AAB63212.

XX New human immune system associated proteins (HISAP) and polynucleotides

PT encoding the HISAP, useful for diagnosing, treating or preventing

PT immune or cell proliferative disorders or infections -

XX Claim 3; Column 87-90; 54pp; English.

CC The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be

CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer.

XX Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;

Query Match 57.7%; Score 192.2; DB 22; Length 891;  
Best Local Similarity 73.6%; Pred. No. 1.2e-45;  
Matches 245; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 cagagatgtgtgactcagccgctccgtgtctgtggtccctggccagaggtctccatc 60  
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 91 cagctcgtccgtgactcagctcgtcgtctgtctgtctgtcgtcgtcgtcgtcgtcgtcgtc 150  
QY 61 acctgtcttgaagcagcagcaacatttgaggttaattgttattgttggctgtaccacag 120  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 151 tctgtacttgaacacagcagtgacatgtgtgtgtatataactatgtctctcgttaccacag 210  
QY 121 gtcccgagatcagcccccagctccatcattagtggtataacacagatcgagctcggggatc 180  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 211 tccccagcagcagcccccaaactcgtatattatgtatgaggtcagtaactcggccctcagggtt 270  
QY 181 cccgacagatctcgcgtccagctcaggtctggtggaacacagcacccctgaccatcagctc 240  
| | | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 271 tctcatcgtctctcgtcgtcctcaagctcgtgcaacacggtccctcgtaccatctcgtggtc 330  
QY 241 caggtctgagagcagcagcagatttactgtgcacgtatataaagttacttaagttgtgtt 300  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 331 caggtctgagagcagcagcagtttacttactgcaactcagatgcagcagcagcaaatgtgtt 390  
QY 301 ttccgacgagcagcagcagcgtcgtcgtgtgt 333  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 391 ttccgagagagcagcagcgtcgtcgtgtgt 423

## RESULT 13

AAQ12840

ID AAQ12840 standard; DNA; 1044 BP.

AC AAQ12840;

DT 17-OCT-1991 (first entry)

XX Variable region of lambda type light chain specific for LPS of

DE Pseudomonas aeruginosa.

XX Monoclonal antibody; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 562..892

FT FT /\*tag= a

FT FT /label= LH

FT FT /note= "Claim 5"

PN JP03151876-A.

PD 28-JUN-1991.

PF 08-NOV-1989; 89JP-0291981.

PR 08-NOV-1989; 89JP-0291981.

PA (SUMO ) SUMITOMO CHEM IND KK.

PA (SUMI-) SUMITOMO SEIYAKU KK.

DR WPI; 1991-234064/32.

DR P-PDB; AAR13184.

Query Match	57.7%	Score 192.2	DB 12	Length 1044
Best Local Similarity	73.6%	Pred. No. 1.3e+45		
Matches 245	Conservative 0	Mismatches 88	Indels 0	Gaps 0

RESULT	14
AAF92354	
ID	AAF92354 standard; cDNA; 464 BP.

DT	15-MAY-2001	(first entry)
DE	Bovine mammary tissue derived cDNA #67.	
XX		
KM	Bovine; mammary gland; cancer; tumour; angiogenesis; ss	
XX		
OS	Bos taurus.	
XX		
PN	W0200114553-A1.	
XX		
PD	01-MAR-2001.	
XX		
PF	23-AUG-2000; 2000WO-NZ00166.	
XX		
PR	23-AUG-1999; 99US-0150330.	
XX		
PA	(GENE-) GENESIS RES & DEV CORP LTD.	
PA	(NAPA-) NEM ZEALAND PASTORAL AGRIC RES INST LTD.	
XX		
PI	Havukkala IJ, Gleen M, Gritgor MR, Molenaar AJ;	
XX		
DR	WPI; 2001-226619/23.	
XX		

PS Claim 1; Page 59; 97pp; English.

SQ Sequence 464 BP; 99 A; 161 C; 120 G; 84 T; 0 other;

RESULT	15
AAH42401	
ID	AAH42401 standard; DNA; 333 BP

DE Nucleotide sequence of variable light chain fragment of clone G93.

KW antibody, light chain; VJ, amyloid protein; blood brain barrier; KW endothelial cell; brain cell antigen; inflammation; adhesion molecule; KW transferrin receptor; neurological disease; Alzheimer's disease; KW prion disease; AIDS-related dementia; epilepsy; brain injury; ss.

OS Homo sapiens.

PN	WO200144300-A2.
XX	
PD	21-JUN-2001.
XX	
PF	27-NOV-2000; 2000WO-GB04501
XX	
PR	13-DEC-1999; 99US-0170599

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Webster C, Osbourn J, Ward G, Miller K;

DR WPI; 2001-398131/42.  
DR P-PSDB; AAG62957.

XX Mixture or panel of antibodies for selecting specific binding members  
PT that cross the blood brain barrier, for use in delivering different  
PT molecules and treating neurological diseases -  
XX

PS Disclosure; Page 103; 109pp; English.

CC The present sequence encodes an antibody variable light chain (VL)  
CC fragment. The fragment is used to produce a mixture or panel of 5  
CC different specific binding members, each comprising an antibody VH  
CC and/or VL variable domain and capable, when displayed on the surface  
CC of filamentous bacteriophage particles or in the case of a specific  
CC binding member comprising the D5 VH and/or VL variable domain when  
CC bound to human serum amyloid protein, to pass through a mammalian  
CC blood brain barrier (BBB). The panel is useful for the selection of  
CC specific binding members with a desired property such as ability to  
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,  
CC ability to bind areas of inflammation in the brain or BBB breakdown or  
CC ability to bind intracellular adhesion molecules and to bind transferrin  
CC receptor. The antibodies are useful in diagnosis, prophylaxis and  
CC treatment of human or animal body, including neurological diseases, such  
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy  
CC and traumatic brain injury and any diseases involving inflammation  
CC occurring within the brain or central nervous system.

XX  
SQ Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 other:

Query Match 56.9%; Score 189.6; DB 22: Length 333;

Best Local Similarity 73.2%; Pred. No. 5.2e-45;

Matches 243; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

OY 1 caggatgtctgactcagccgtctctcgtgctcctggtccctggccagaggtccatc 60  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 cagtcgtgtctgactcagctcgtctcgtctggtctctctgacagtcacacacac 60  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
OY 61 acctgctcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 tctctgactcggagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
OY 121 gtccacagatcagcccccagactcctcatcagtgctacacacagcagcctcg 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 caccacagcaagcccccacacatcatgatgatgagcgagtaagcgccctcag 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
OY 181 ccgagcagattctcggctcaggtctgtggaacacagccactgaccatcagctgc 240  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 181 tctaatcgtctctctgctccaaagtctggcaacacgctccctgacaatctgtgctc 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
OY 241 caggtcgaagcagagcagattatctatctgcatcgtatcaagtaacttactagtg 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 241 caggtcgaagcagagcaggtatattactgcatcgtatcaatacaacagggagcactc 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
OY 301 ttccgacgcggagcagcagcagcagcagcagcagcagcagcagcagcagcag 332  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 301 ttccgacgcggagcagcagcagcagcagcagcagcagcagcagcagcagcag 332  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: August 11, 2002, 22:10:21  
Job time: 7701 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 22:03:49 ; Search time 1984.69 Seconds  
(without alignments)  
3511.146 Million cell updates/sec

Title: US-09-786-015-3

Perfect score: 333  
Sequence: 1 cagatgtgtctgactcagcc.....ccaggtgcacgcctctggt 333

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl:

1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_pr:\*  
10: gb\_to:\*  
11: gb\_sy:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgc\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	272.2	81.7	333	4	AF172689	AF172689 Ovis arle
2	269.4	80.9	393	4	BTU32261	U32261 Bos taurus
3	269	80.8	333	4	AF172684	AF172684 Ovis arle
4	267.4	80.3	333	4	AF172691	AF172691 Ovis arle
5	267.4	80.3	333	4	AF172693	AF172693 Ovis arle
6	265.8	79.8	333	4	AF172690	AF172690 Ovis arle
7	261.4	78.5	393	4	BTU31106	U31106 Bos taurus
8	261	78.4	333	4	AF172697	AF172697 Ovis arle
9	259.8	78.0	393	4	BTU32249	U32249 Bos taurus
10	259.8	78.0	393	4	BTU32254	U32254 Bos taurus
11	259.6	78.0	330	4	AF015797	AF015797 Bos taurus
12	259.4	77.9	333	4	AF172695	AF172695 Ovis arle
13	257.8	77.4	330	4	AF172687	AF172687 Ovis arle
14	257.6	77.4	336	4	AF172688	AF172688 Ovis arle
15	256.2	76.9	330	4	AF172696	AF172696 Ovis arle
16	254.8	76.5	538	4	AF040919	AF040919 Ovis arle
17	254.4	76.4	336	4	AF172698	AF172698 Ovis arle
18	253.2	76.0	330	4	AF015796	AF015796 Bos taurus
19	253	76.0	330	4	AF172686	AF172686 Ovis arle
20	253	76.0	333	4	AF172682	AF172682 Ovis arle
21	251.4	75.5	333	4	AF015795	AF015795 Bos taurus
22	251.4	75.5	333	4	AF015801	AF015801 Bos taurus
23	249.8	75.0	333	4	AF015798	AF015798 Bos taurus
24	248.6	74.7	399	4	BTU32250	U32250 Bos taurus
25	248.2	74.5	330	4	AF172692	AF172692 Ovis arle
26	248.2	74.5	333	4	AF015799	AF015799 Bos taurus
27	248.2	74.5	333	4	AF172701	AF172701 Ovis arle
28	246.6	74.1	333	4	AF015791	AF015791 Bos taurus
29	246.6	74.1	333	4	AF015792	AF015792 Bos taurus
30	246.6	74.1	333	4	AF015793	AF015793 Bos taurus
31	246.6	74.1	333	4	AF172683	AF172683 Ovis arle
32	245.2	73.6	336	4	AF023841	AF023841 Bos taurus
33	245.2	73.6	632	4	AF040920	AF040920 Ovis arle
34	245	73.6	339	4	AF172685	AF172685 Ovis arle
35	243.4	73.1	333	4	AF015800	AF015800 Bos taurus
36	243.4	73.1	333	4	BTU012799	U32255 Bos taurus
37	242.6	72.9	393	4	BTU32255	U32255 Bos taurus
38	242.2	72.7	368	4	BTU32264	U32264 Bos taurus
39	242	72.7	629	4	AF040916	AF040916 Ovis arle
40	241.8	72.6	333	4	BTU012801	U32264 Bos taurus
41	241.8	72.6	339	4	AF172694	AF172694 Ovis arle
42	241.6	72.6	336	4	AF172699	AF172699 Ovis arle
43	240.4	72.2	629	4	AF040909	AF040909 Ovis arle
44	240	72.1	336	4	BTU012802	U32254 Bos taurus
45	238.6	71.7	330	4	AF023843	AF023843 Bos taurus

#### ALIGNMENTS

RESULT 1  
AF172689  
LOCUS AF172689 333 bp mRNA linear MAM 29-AUG-1999  
DEFINITION Ovis aries clone 34 immunoglobulin light chain variable region  
(IGLV) mRNA, partial cds.  
ACCESSION AF172689  
VERSION AF172689.1 GI:5802425  
KEYWORDS  
SOURCE  
ORGANISM

sheep.  
Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
REFERENCE  
1 (bases 1 to 333)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
nematode parasite Haemonchus contortus

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 333)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
Direct Submission  
Submitted (26-JUL-1999) School of Veterinary Science, The Centre

for Animal Biotechnology, The University of Melbourne, Parkville,  
Melbourne, Victoria 3052, Australia

# FEATURES

source

1..333  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
/clone="34"  
/tissue\_type="abomasal lymph node"

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/gene="IGLV"  
<1..>333  
/gene="IGLV"  
/codon\_start=1  
/product="immunoglobulin light chain variable region"  
/protein\_id="AAD51679.1"  
/db\_xref="GI:5802426"  
/translation="QAVLTQPSVSRSLGQSVSYNCGSSNIGYVSWVQVQVGS  
APKIIYGTATSRASGIPDRFSSRGNTATLTLSLQAGDESDYICASYQDDSEIRG  
SGRTLVIG"

CDS

BASE COUNT 68 a 97 c 91 g 77 t  
ORIGIN

Query Match 81.7%; Score 272.2; DB 4; Length 333;  
Best Local Similarity 88.6%; Pred. No. 2e-63; Indels 0; Gaps 0;

Matches 295; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

1 cagagatgctgactcagcgcgtcctcgtgctggtgctcctgagcagaggtctcacc 60

1 CAGAGGTGCTGACTCAGCAGCGTCCGTCCGTCACAGTCCCTGGCCAGAGTGTTCATC 60

61 accgtctctggaagcagcagcaacattggaggtaatgcttatgtggtctgtcacaacag 120

61 ACCTGCTCTGGAGAGCAGCAGCAACATGGATATGGTAATATGTAGCTGTACCAACAG 120

121 gtcccaagatcagcccccagactccctcagtcagtcacacagatcagcctcggagatc 180

121 GTCCCAAGATCAGCCCCAGACTCCCTCAGTCAGTCACACAGATCAGCCTCGGAGATC 180

181 cccgagacgatctcgcgtctcaggtctgggaacacagcaccctgacacatcagctcgtc 240

181 CCCGAGACGATCTCGCGTCTCAGGTTGGCAGACAGCAGCATTGTGACATCAGCTCGG 240

241 caggtctggaagcagcagcagcattggtggtggtggtggtggtggtggtggtggtggt 300

241 CAGGCTGGAGCAGAGTCCGATTATGCTGCTCTATACAGATGATGACAGTGAATG 300

301 ttcgcaagcggagcagcagcgtgacgtctggtggt 333

301 TTCCGAGCGGAGCAGCAGCTGACCGTCTGGGT 333

RESULT 2  
BTU32261 393 bp mRNA linear MAM 25-APR-1996

DEFINITION Bos taurus clone 16 immunoglobulin lambda light chain variable

region (Vlamdala) mRNA, partial cds.

U32261 GI:1276622

ACCESION U32261.1 GI:1276622

VERSION U32261.1 GI:1276622

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 393)

Ivanov,V.N., Karginov,V.A., Morozov,I.V. and Gorodetsky,S.I.

Molecular cloning of a bovine immunoglobulin lambda chain cDNA

Gene 67 (1), 41-48 (1988)

88329743

2 (bases 1 to 393)

Jackson,T., Morris,B.A. and Sanders,P.G.

Nucleotide sequences and expression of cDNAs for a bovine

anti-testosterone monoclonal IgG1 antibody  
Mol. Immunol. 29 (5), 667-676 (1992)

# JOURNAL

92261635

3 (bases 1 to 393)

Sinclair,M.C., Gilchrist,J. and Aitken,R.

Molecular characterization of bovine V lambda regions

J. Immunol. 155 (6), 3068-3078 (1995)

95403981

4 (bases 1 to 393)

Aitken,R.

Direct Submission

Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of

Biomedical and Life Sciences, University of Glasgow, Joseph Black

Building, Glasgow G12 8QQ, UK

location/Qualifiers

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/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone="16"

/cell\_type="lymphocyte"

/tissue\_type="spleen"

/dev\_stage="adult"

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/gene="Vlamdala"

1..66

/gene="Vlamdala"

1..>393

/gene="Vlamdala"

/note="Vlamdala family, group c"

/codon\_start=1

/product="immunoglobulin lambda light chain variable

region"

/protein\_id="AAC48561.1"

/db\_xref="GI:1276623"

/translation="MSTAMSPILITIVICTGSMQAVLTQPSVSGSLGQVSYNC

SGSSNVGCTGVSWVQVQVIRGAPRTLLTGATSRASGVDPDRFSSRGNTATLTITSL

QAEADADYFCASYSQSSNTAVFSGTTLV"

67..>393

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/note="Vlamdala family, group c"

/product="immunoglobulin lambda light chain variable

region"

67..132

/gene="Vlamdala"

/note="encodes framework region 1"

133..174

/gene="Vlamdala"

/note="encodes complementarity-determining region 1"

175..219

/gene="Vlamdala"

/note="encodes framework region 2"

220..240

/gene="Vlamdala"

/note="encodes complementarity-determining region 2"

241..336

/gene="Vlamdala"

/note="encodes framework region 3"

337..366

/gene="Vlamdala"

/note="encodes complementarity-determining region 3"

367..393

/gene="Vlamdala"

/note="encodes framework region 4"

BASE COUNT 74 a 132 c 105 g 82 t

ORIGIN

Query Match 80.9%; Score 269.4; DB 4; Length 393;

Best Local Similarity 89.0%; Pred. No. 1.1e-62;

Matches 291; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

1 cagagatgctgactcagcgcgtcctcgtgctggtgctcctgagcagaggtctcacc 60

|||||

Db 67 CAGGCTGTGCTACTACGACCCGCTCTCCGTGTCGGGGTCCCTGGGCGACAGAGGGTCTCCATC 126  
Oy 61 accctctctggaagcagcagaacatitgaggtlaatgctatgtggctggtacacaacg 120  
Db 127 ACCTGCTCTGGAGACGACGACACGTTGGACTGGCAATTATGTAAGCTGGTTCACACG 186  
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcagaccccgaggatc 180  
Db 187 ATCCAGAGATGCGGCCGCCAGAACCCCTCANTCTATGTGTCGACAGTCGAGCCTCGGGGTC 246  
Oy 181 cccgacagatctcccgctcaggtctcggaaacacagccaccctgacatcagctcgtc 240  
Db 247 CCCGACCATTCCTCCGGCTCCAGGTCGTGGACACAGCCACCTGACCATCAGTCGCTC 306  
Oy 241 caggtctggaagcagcagatattactcgtgcatcgtatcaagaactactacagtggtgt 300  
Db 307 CAGGCTGAGAGAGAGGACGACATATTCTGTGCTCATCTTATCAGATGATACACACCTGTG 366  
Oy 301 ttccgacagcggagaccaggtcagcgc 327  
Db 367 TTCGGCAGCGGAGCACACTGACGCTC 393

## RESULT 3

AF172684 333 bp mRNA linear MAM 29-AUG-1999  
LOCUS Ovis aries clone 17 immunoglobulin light chain variable region  
DEFINITION (IGLV) mRNA, partial cds.

ACCESSION AF172684 GI:5802415

VERSION AF172684.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

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AUTHORS

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AUTHORS

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JOURNAL

Oy 1 caggatgtctactcagccgctccctcgtgtcgttgggtccctcgggccaagaggtccacc 60  
Db 1 CAGGCTGTGCTACTACGACCCGCTCTCCGTGTCGGGGTCCCTGGGCGACAGAGGGTCTCCATC 60  
Oy 61 accctctctggaagcagcagaacatitgaggtlaatgctatgtggctggtacacaacg 120  
Db 61 ACCTGCTCTGGAGACGACGACACGTTGGACTGGCAATTATGTAAGCTGGTTCACACG 120  
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcagaccccgaggatc 180  
Db 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcagaccccgaggatc 180  
Oy 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcagaccccgaggatc 180  
Db 121 gtcccaagatcagcccccagactcctcatcagtgctacacagatcagaccccgaggatc 180  
Oy 181 cccgacagatctcccgctcaggtctcggaaacacagccaccctgacatcagctcgtc 240  
Db 181 CCCGACCATTCCTCCGGCTCCAGGTCGTGGACACAGCCACCTGACCATCAGTCGCTC 240  
Oy 241 caggtctggaagcagcagatattactcgtgcatcgtatcaagaactactacagtggtgt 300  
Db 241 CAGGCTGAGAGAGAGGACGACATATTCTGTGCTCATCTTATCAGATGATACACACCTGTG 300  
Oy 301 ttccgacagcggagaccaggtcagcgc 333  
Db 301 TTCGGCAGCGGAGCACACTGACGCTC 393

## RESULT 4

AF172691 333 bp mRNA linear MAM 29-AUG-1999  
LOCUS Ovis aries clone 81 immunoglobulin light chain variable region  
DEFINITION (IGLV) mRNA, partial cds.

ACCESSION AF172691 GI:5802429

VERSION AF172691.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

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JOURNAL

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AUTHORS

TITLE

Query Match 80.3%; Score 267.4; DB 4; Length 333;  
Best Local Similarity 87.7%; Pred. No. 4e-62;  
Matches 293; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Query Match	80.3%	Score 267.4	DB 4	Length 333	
Best Local Similarity	87.7%	Pred. NO. 4e-62			
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OY	1	cagaagtcgtctaacacagccgtctccgtctgtcttgatccctctggagcaagagttccatc	60		
Db	1	CAGGCTGTGCTTACTACACGCCGTCTCCGTGCCAAGTCCCTTGSGCCAGAGGGTCTCCATC	60		
OY	61	acctgtctctggaagcagcagcaacatctgagtgtaattgtattatgttgctgtgtaccaaag	120		
Db	61	ACCTGCTCTGGAAGCAGCAGCAACGTTGGATATGTGTAATTAATGTGGGCTGTATCAACAG	120		
OY	121	gtcccaagatcaagcccccaagactccctcatcaagtgtctaaacccatctgagcctctggagtc	180		
Db	121	GTCCCAAGATCAGCCCCCAAACTCTCATTTTATGTGTGCACCCGTCTGAGCCCTCGGGGGGTTC	180		
OY	181	ccggaccgaattctccggtctccagtccttggaacacagcaccccttaccatctagctctgcgtc	240		
Db	181	CCGGACCGAATTCCTCGGCTCCAGGTCTGGCAACAACAGCAGCATCTTACCATCAGCTCGCTC	240		
OY	241	caagcttgaggaagcagccgatattactcgttgatcgtctatcaaaagtactaacagtgtgt	300		
Db	241	CAGGCTGAGAGCAGAGCCGATATTATCTCTGATTTTATGACCAAGGTAAGTTGGGGGTGT	300		
OY	301	ttcggcaagcggagaccagagctgaccgtctcctgggt	333		

RESULT	6
LOCUS	AF172690
DEFINITION	AF172690 Ovis aries clone 100 immunoglobulin light chain variable region (IGLV) mRNA, partial cds.
ACCESSION	AF172690
KEYWORDS	AF172690.1 GI:5802427
SOURCE	sheep.
ORGANISM	Ovis aries
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
AUTHORS	1 (bases 1 to 333)
TITLE	White, G.P., Meusen, E.N.T. and Newton, S.E. A single-chain variable region immunoglobulin library from the abomasal lymph node of sheep infected with the gastrointestinal nematode parasite Haemonchus contortus
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 333)
AUTHORS	White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUL-1999) School of Veterinary Science, The Centre for Animal Biotechnology, The University of Melbourne, Parkville, Melbourne, Victoria 3052, Australia
FEATURES	location/Qualifiers
source	1..333
	/organism="Ovis aries"
	/db_xref="taxon:9940"
	/clone="100"
	/tissue_type="abomasal lymph node"
	1..333
gene	/gene="IGLV"
	<1..>333
CDS	/gene="IGLV"
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	/protein_id="AAD51680.1"
	/db_xref="GI:5802428"
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ORIGIN	

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/note="from the V11 family group; similar to product
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SOURCE	sheep.
ORGANISM	Ovis arles

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 333)  
 White, G.P., Meusen, E.N.T. and Newton, S.E.  
 A single-chain variable region immunoglobulin library from the abomasal lymph node of sheep infected with the gastrointestinal nematode parasite *Haemonchus contortus*  
 Unpublished  
 2 (bases 1 to 333)  
 White, G.P., Meusen, E.N.T. and Newton, S.E.  
 Direct Submission  
 Submitted (26-JUL-1999) School of Veterinary Science, The Centre for Animal Biotechnology, The University of Melbourne, Parkville, Melbourne, Victoria 3052, Australia  
 Location/Qualifiers  
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 /organism="Ovis aries"  
 /db\_xref="taxon:9940"  
 /clone="58"  
 /cissue="58"  
 /cissue\_type="abomasal lymph node"  
 1..333  
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 /gene="IGLV"  
 /codon\_start=1  
 /product="Immunoglobulin light chain variable region"  
 /protein\_id="AAD51687.1"  
 /db\_xref="GI:5802442"  
 /translation="QAVLPSSVSLGQSVSLGSSSSNVGIDYGVYQOVPKGS  
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 SGTRLTVLG"  
 BASE COUNT 64 a 95 c 92 g 82 t  
 ORIGIN  
 Query Match 78.4%; Score 261; DB 4; Length 333;  
 Best Local Similarity 86.5%; Pred. No. 2.2e-60;  
 Matches 288; Conservative 0; Mismatches 45; Indels 0; Gaps 0;  
 QY 1 caggatgtctgactcagccgctccctcgtctcgtggtccctgagccagaggtctccatc 60  
 Db 1 CAGGCTGTGCTGACTCAGCCGCTCCTCGTCCAGTCCCTGGCCAGAGTGTCTCATC 60  
 QY 61 acctgctctggaagcagcagaacattggaagttaatgltatgltggctggtaccacag 120  
 Db 61 ACCTGCTCTGGAAGCAGACAGCAAGTGTGATTTGATGATGAGGCTGTGACCAACAG 120  
 QY 121 gtccagagatcacagcccgagctccatcagtgtctacacagcagatcgagctcggtgac 180  
 Db 121 GTCCAGAGATCACGCCCAACTCTCATTTATGTGTCACACAGTCCGCTCGGGGCTC 180  
 QY 181 ccgagaccatctccgagctcaggtctggaacacagccaccctgaccacagctcgctc 240  
 Db 181 CCGAGACGATTTTCGCGCTCCAGGTTTGGCAACACAGCACTTATTTATCAATTCGCTC 240  
 QY 241 caggctgaggaagcagagccgattactgtgcactcgatcaaaagttacttacagtggtt 300  
 Db 241 CAGGCTGAGGAGCAGGCGGATTTACTGTGATCTGTGACAGTACTGACGGTACTATT 300  
 QY 301 ttgcgacgaggaagcaggtcgacgctctggt 333  
 Db 301 TTGCGCAGTGGGACAGGCTGACCGTCTGGGT 333  
 RESULT 9  
 BFN32249 393 bp mRNA linear MAM 25-APR-1996  
 LOCUS BFN32249 393 bp mRNA linear MAM 25-APR-1996  
 DEFINITION Bos taurus clone 2 immunoglobulin lambda light chain variable  
 region (Vlambda) mRNA, partial cds.  
 ACCESSION U32249  
 VERSION U32249.1 GI:1276598  
 KEYWORDS

SOURCE  
 ORGANISM cow.  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.  
 1 (bases 1 to 393)  
 Ivanov, V.N., Karginov, V.A., Morozov, I.V. and Gorodetsky, S.I.  
 Molecular cloning of a bovine immunoglobulin lambda chain cDNA  
 Gene 67 (1), 41-48 (1988)  
 88329743  
 MEDLINE  
 JOURNAL  
 2 (bases 1 to 393)  
 Jackson, T., Morris, B.A. and Sanders, P.G.  
 Nucleotide sequences and expression of cDNAs for a bovine anti-testosterone monoclonal IgG1 antibody  
 Mol. Immunol. 29 (5), 667-676 (1992)  
 92261635  
 MEDLINE  
 JOURNAL  
 3 (bases 1 to 393)  
 Sinclair, M.C., Gilchrist, J. and Aitken, R.  
 Molecular characterization of bovine V lambda regions  
 J. Immunol. 155 (6), 3068-3078 (1995)  
 95403981  
 MEDLINE  
 REFERENCE  
 4 (bases 1 to 393)  
 Aitken, R.  
 Direct Submission  
 Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of Biomedical and Life Sciences, University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  
 Location/Qualifiers  
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 /protein\_id="AAC48549.1"  
 /db\_xref="GI:1276599"  
 /translation="MSTMAVPLILVLTGSMNAQAVLTQPSVSGVLTGQVSLTSC  
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 QADEADYFCASITGTNTAIFSGITLV"  
 67..>393  
 /gene="Vlambdaa"  
 /note="Vlambda family, group a"  
 /product="Immunoglobulin lambda light chain variable region"  
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 /note="encodes framework region 1"  
 133..174  
 /gene="Vlambdaa"  
 /note="encodes complementarity-determining region 1"  
 175..219  
 /gene="Vlambdaa"  
 /note="encodes framework region 2"  
 220..240  
 /gene="Vlambdaa"  
 /note="encodes complementarity-determining region 2"  
 241..336  
 /gene="Vlambdaa"  
 /note="encodes framework region 3"  
 337..366  
 /gene="Vlambdaa"  
 /note="encodes complementarity-determining region 3"

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                /note="encodes framework region 4"
BASE COUNT      79 a      130 c      99 g      85 t
ORIGIN
Query Match      78.0%; Score 259.8; DB 4; Length 393;
Best Local Similarity 87.2%; Pred. No. 4.6e-60;
Matches 285; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 caggatgtgctgactcagccgctcctcgtgctggttccttcggcagagggctccatc 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 67 CAGGCTGTGCTGACTACAGCCGTCCTCCGTCGGGTACTGGCCAGAGGCTCCATC 126

QY 61 acctctctggaagcagcagcaacattggaggtaatgtcttatgtggtctgtacacag 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 127 ACCTGCTGTGAAGCAGCGCAACGTTGGAGTGGCAATTATGTGAGCTGTCCAAACAG 186

QY 121 gtccagagatcagcccccagactcctcatcagtgctgtacacagatcagagctcgggagtc 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 ATCCAGAGATCAGCCCCCAAAACCTCATCTATGATGCGACCAAGTCGAACCTGGGGGTC 246

QY 181 ccgagaccgattctccggtctcaggtctggtggaacacagccaccctgaccatcagctgcgc 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 247 CCCGACCATCTCTCCGGGCTCCAGGTCGTGGGAAGCTCAGCCACCTGATGATCAGCTCGTC 306

QY 241 caggctgagagcagagccgattactatctgcatcgtatcaagaactacagtggtgtt 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 CAGGCTGAGAGCAGGCGGATTTATTTGTGTCATCTTAACTGTAACACAGCTATT 366

QY 301 ttcggcagcgagcagcagcagctgacgctc 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 367 TTCGGCAGCGGAAACCACTGACCGTC 393

RESULT 10
BTU32254      393 bp      mRNA      linear      MAM 25-APR-1996
LOCUS
DEFINITION   Bos taurus clone 8 Immunoglobulin lambda light chain variable
                region (Vlambdala) mRNA, partial cds.
ACCESSION   U32254
VERSION     U32254.1 GI:1276608
KEYWORDS
SOURCE
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 393)
            Ivanov,V.N., Karginov,V.A., Morozov,I.V. and Gorodetsky,S.I.
            Molecular cloning of a bovine Immunoglobulin lambda chain cDNA
            Gene 67 (1), 41-48 (1988)
JOURNAL     88329743
MEDLINE     88329743
REFERENCE   2 (bases 1 to 393)
            Jackson,T., Morris,B.A. and Sanders,P.G.
            Nucleotide sequences and expression of cDNAs for a bovine
            anti-testosterone monoclonal IgG1 antibody
            Mol. Immunol. 29 (5), 667-676 (1992)
JOURNAL     92261635
MEDLINE     92261635
REFERENCE   3 (bases 1 to 393)
            Sinclair,M.C., Gilchrist,J. and Aitken,R.
            Molecular characterization of bovine V lambda regions
            J. Immunol. 155 (6), 3068-3078 (1995)
JOURNAL     95403981
MEDLINE     95403981
REFERENCE   4 (bases 1 to 393)
            Aitken,R.
            Direct Submission
            Submitted (25-JUL-1995) Robert Aitken, Microbiology, Institute of
            Biomedical and Life Sciences, University of Glasgow, Joseph Black
            Building, Glasgow G12 8QQ, UK
JOURNAL
TITLE
AUTHORS
FEATURES
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QY 121 gtccagagatcagcccccagactcctcatcagtgctgtacacagatcagagctcgggagtc 180
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QY 181 ccgagaccgattctccggtctcaggtctggtggaacacagccaccctgaccatcagctgcgc 240
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Db 307	CAGGCTGAGGACGACGACGATTATTTCGTGCGGGCTTATCCAGGGTGTAACACAGCTGTT	366									
QY 301	ttcggcagcgggagccagcgtcagctc 327										
Db 367	TTTCGGCAGCGGGACACACATGATGCTC 393										
RESULT 11											
LOCUS	AF015797	330 bp	mRNA	linear	MAM 12-AUG-1997						
DEFINITION	Bos taurus immunoglobulin light chain variable region mRNA, partial cds.										
ACCESSION	AF015797										
VERSION	AF015797.1	GI:2323383									
KEYWORDS											
SOURCE	cow.										
ORGANISM	Bos taurus										
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.										
AUTHORS	1 (bases 1 to 330)										
TITLE	Saini, S.S., Jacobs, R. and Kaushik, A.										
JOURNAL	Structural features of immunoglobulin variable-region lambda light chain of BLV-infected cattle										
REFERENCE	2 (bases 1 to 330)										
AUTHORS	Saini, S.S., Jacobs, R. and Kaushik, A.										
TITLE	Direct Submission										
JOURNAL	Submitted (24-JUL-1997) Pathobiology, University of Guelph, ON N1G 2W1, Canada										
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QY 121	gtccagagatacagcccccagactcctcatcagtgctactacaaccagatcgagcctcgggatac 180										
Db 121	ATCCGAGATCGGGCCCCCAAGAACCTCATCTATGATGTCGACACAGTCGAGCCCTCGGGGGTC 180										
QY 181	ccgaacgcatctccgaggtcaggtctgggaagaagcacccttgacaacatcagctcgctc 240										
Db 181	CCCCAGCCATTTCTCCGGCTCCAGGCTGTGGGAACACAGCCACCCTGACCATCATCAGCTGCTC 240										

QY	301	ttcgccagcggagccagcgtcacgcctctg	330
Db	301	ttcgccagcggagccagcgtcacgcctctg	330
RESULT 12			
LOCUS	AF172695	333 bp	mRNA
DEFINITION	Ovis aries clone 96 immunoglobulin light chain variable region (IGLV) mRNA, partial cds.		
ACCESSION	AF172695		
VERSION	AF172695.1		
KEYWORDS	GI:5802437		
SOURCE	Sheep.		
ORGANISM	Ovis aries		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.		
AUTHORS	1 (bases 1 to 333)		
TITLE	White,G.P., Meusen,E.N.T. and Newton,S.E.		
JOURNAL	A single-chain variable region immunoglobulin library from the abomasal lymph node of sheep infected with the gastrointestinal nematode parasite Haemonchus contortus		
REFERENCE	unpublished		
AUTHORS	2 (bases 1 to 333)		
TITLE	White,G.P., Meusen,E.N.T. and Newton,S.E.		
JOURNAL	Direct Submission		
FEATURES	Submitted (26-JUL-1999) School of Veterinary Science, The Centre for Animal Biotechnology, The University of Melbourne, Parkville, Melbourne, Victoria 3052, Australia		
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QY	181	ccgacacgaattcccgctcaggtctcaggtcttgggaacacagccaccctgacatcagctcgtc	240
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QY	241	caggtctgagcagagccgagatattacttgtgatcatgatacaagtaactacagttggtgt	300



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DEFINITION Ovis aries clone 146 immunoglobulin light chain variable region  
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ACCESSION AF172687  
VERSION AF172687.1 GI:5802421  
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Bovidae; Caprinae; Ovis.  
REFERENCE 1 (bases 1 to 330)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
nematode parasite Haemonchus contortus  
Unpublished  
2 (bases 1 to 330)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
Direct Submission  
Submitted (26-JUL-1999) School of Veterinary Science, The Centre  
for Animal Biotechnology, The University of Melbourne, Parkville,  
Melbourne, Victoria 3052, Australia  
JOURNAL  
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AUTHORS  
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Oy 241 caggctggaagcagagcccgattactgtgcatcgtatcaagaactcactcaagtggtgt 300  
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Oy 301 ttcgcagcgggacagcgtctgacctgctggt 333  
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(IGLV) mRNA, partial cds.  
ACCESSION AF172688  
VERSION AF172688.1 GI:5802423  
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SOURCE sheep.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Bovidae; Caprinae; Ovis.  
REFERENCE 1 (bases 1 to 336)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
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Unpublished  
2 (bases 1 to 336)  
White, G.P., Meusen, E.N.T. and Newton, S.E.  
Direct Submission  
Submitted (26-JUL-1999) School of Veterinary Science, The Centre  
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Melbourne, Victoria 3052, Australia  
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AUTHORS  
TITLE  
JOURNAL  
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Oy 181 cccgacagatcttcggcgtccagagtgctggaacaacagcacccctgacatcgctgcgc 240  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 19:45:49 ; Search time 2546.98 Seconds  
(without alignments)  
1923.609 Million cell updates/sec

Title: US-09-786-015-1

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Scoring table: IDENTITY\_NUC  
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Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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1: em\_esthba:\*  
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6: em\_esttpl:\*  
7: em\_estvro:\*  
8: em\_hlc:\*  
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11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
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15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	246	67.8	509	10	BE480721 165931 BA
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4	242	66.7	555	9	AV667743
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7	236.2	65.1	456	10	BE481532 167023 BA
8	235.4	64.8	492	10	BE692159 341738 BA
9	235.4	64.8	583	10	BE846118 232255 BA
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20	229.4	63.2	441	10	BE485653 172779 BA
21	229.2	63.1	514	10	BE480296 165337 BA
22	229	63.1	413	10	BE481411 166849 BA
23	228.2	62.9	547	10	BE692467 342167 BA
24	228	62.8	396	10	BE230754 252610 BA
25	227.4	62.6	502	10	BE485914 173210 BA
26	227	62.5	598	10	BE588390 194071 BA
27	226.8	62.5	397	10	BE487323 176001 BA
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30	225.4	62.1	462	10	BE692835 342677 BA
31	225.2	62.0	516	10	BE690115 385440 BA
32	224.2	61.8	409	10	BE482642 168491 BA
33	224.2	61.8	549	10	BE845758 232868 BA
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37	223.8	61.7	503	10	BE485219 172170 BA
38	223.6	61.6	390	10	BE482316 168057 BA
39	223.6	61.6	498	10	BE484853 171651 BA
40	223.6	61.6	512	10	BE482341 168089 BA
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42	223.4	61.5	497	10	BE486006 173340 BA
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DEFINITION 160120 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE476735  
VERSION BE476735.1 GI:9596268

KEYWORDS  
SOURCE  
ORGANISM

Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE  
1 (bases 1 to 489)  
Sonstegard,R.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

AUTHORS

TITLE  
JOURNAL  
COMMENT  
Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414

Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
V0.980904.e. Vector identified by cross-match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACGCTATGACAT  
BACKWARD: GTTTCACGACGACG  
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FEATURES  
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and -mismatch 12 options.

PCR Primers

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BACKWARD: GTTTCCCACTACAGAG

Plate: 137 row: A column: 22

Seq primer: ATTAGTGACACTATAG.

#### FEATURES

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/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site1: XbaI; Site2: XhoI;

Library made from pooled mRNA isolated from mammary

tissues at eight physiological, developmental, and disease

states."

BASE COUNT

106 a 161 c 131 g 111 t

ORIGIN

Query Match

Best Local Similarity 67.4%; Score 244.6; DB 10; Length 509;

Matches 289; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

```

Oy 1 caggtagcagctcagagatcgagaccagccctggtgaagccctcaagaccctctccctc 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 73 CAGGTGACACTCGGGAGTCGGGCCCCCAGCTGTGTAAGCCCTCACAGACCTCTCCCTC 132
Oy 61 accctcagcgtctcgtatctcattcaacaaagatagtgtgtatgtgtgtgtgtgtgt 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 133 ACCTGACAGCTCTGTGATTCATTGATGATGATGATGATGATGATGATGATGATGATG 192
Oy 121 cagagaagagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 180
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 193 CCAGAAAGGCGCTGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 252
Oy 181 aacagccctacagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 253 CCAGCCCTGAATCCCGGCTGACATCACCAGACCAACTCCGTGAGCCAACTCTCTG 312
Oy 241 tcactgagcagcgtgactactcagagacagcagcagcagcagcagcagcagcagcag 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 313 TCAGTAGAGCTGTGACAACTGAGGACAGCCACATCTATTGTGCGAAGCATCTACT 372
Oy 301 ggtgacagtggtccttaagtgttgacactcagagccagcagcagcagcagcagcag 360
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 373 GTAGTTGTTATGCTGTAACGTGATGCTGGGCGCAAGGACTCCTGCTCACCGTCTCC 432
Oy 361 tca 363
    |||
Db 433 TCA 435

```

#### RESULT 4

AV667743 555 bp mRNA linear EST 28-NOV-2001

LOCUS AV667743 Bos taurus ovary fetus Bos taurus cDNA clone E10V017E06

DEFINITION 5', mRNA sequence.

ACCESSION AV667743

VERSION AV667743.1 GI:9932488

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 555)

Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.

Establishment of a high throughput EST sequencing system using

poly(A) tail-removed cDNA libraries and determination of 36,000

bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)

COMMENT 21570554

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugi@cocoa.ocn.ne.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

#### FEATURES

source

1..555

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone="E10V017E06"

/clone\_lib="Bos taurus ovary fetus"

/tissue\_type="ovary"

/dev\_stage="fetus"

/lab\_host="DH10B"

/note="Vector: pZL1; Site1: SalI; Site2: NotI; Poly A

was deleted from a NotI site"

BASE COUNT 113 a 173 c 148 g 119 t 2 others

ORIGIN

Query Match

Best Local Similarity 66.7%; Score 242; DB 9; Length 555;

Matches 297; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

```

Oy 1 caggtagcagctcagagatcgagaccagccctggtgaagccctcaagaccctctccctc 60
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 90 CAGGTGACACTCGGGAGTCGGGCCCCCAGCTGTGTAAGCCCTCACAGACCTCTCCCTC 149
Oy 61 accctcagcgtctcgtatctcattcaacaaagatagtgtgtatgtgtgtgtgtgtgt 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 150 ACCTGACAGCTCTGTGATTCATTGATGATGATGATGATGATGATGATGATGATGATG 209
Oy 121 cagagaagagcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 180
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 210 CCAGGAGGCGCTGAGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 269
Oy 181 aacagccctacagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 270 CCAGCCCTGAATCCCGGCTGACATCACCAGACCAACTCTTAAGCCCAAGTCTCTG 329
Oy 241 tcactgagcagcgtgactactcagagacagcagcagcagcagcagcagcagcagcag 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 330 TCAGTAGAGCTGTGACAACTGAGGACAGCCACATCTACTACTGTGAAAGGATGTAT 389
Oy 301 ggtgacagtggtccttaagtgt-----tggactactgagccagagcagcagcagcag 354
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 390 GATGCTGATTTATTCATTTGTGAAAACATCGATGCTGGGCGCAAGGACTCTGTCACC 449
Oy 355 gctcctca 363
    |||||||
Db 450 GTCTCTCTNA 458

```

#### RESULT 5

BE487301 504 bp mRNA linear EST 28-AUG-2000

LOCUS BE487301 BE487301 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION BE487301

ACCESSION BE487301.1 GI:9606834

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 504)

Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and

TITLE  
JOURNAL  
COMMENT

Wells, K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -minscore 18 and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCAGTCACGACG  
Plate: 123 row: J column: 18  
Seq primer: ATTTAGTGACCTATAC.  
Location/Qualifiers  
1..504  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 109 a 163 c 128 g 104 t  
ORIGIN

Query Match 66.5%; Score 241.4; DB 10; Length 504;  
Best Local Similarity 79.1%; Pred. No. 7.2e-56;  
Matches 287; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 caggtgcagctcgaagagtcggagaccagctggtgaagccctcacagaccctctccctc 60  
|||||  
DB 80 CAGGTGCACCTCGCGAGTCGGGCCCCAGCCTGTGTAAAGCCCTCACAGACCTCTCCCTC 139  
61 acctgcagctctcgtgattcattcaaccaagatggtgtgagtggttcgcgagagct 120  
|||||  
DB 140 ACCTGCACCATCTCTGGATTCTCATTTGACCACTATGCTGTAACTGTGGGTCGCCAGGCT 199  
QY 121 ccaggaagaagcgcttgagtgagctaggtggtggtccagtggtgacctaaagcctaacc 180  
|||||  
DB 200 CCAGGGAAGGCGCTGGAGTGGCTTGTGTAGTATGACAGTAGTGGAACACAGACTATGCC 259  
QY 181 acagccctacagtcgccgaactcagcgtcaccaaggagacacctccaagaagccaattctccctg 240  
|||||  
DB 260 CCAGCCCTGAATAATCCGCGCTCAGACATCACCAAGGACCAAGCTCCAAGGCCACTCTCTG 319  
QY 241 tcaactgagcagctgagctactcagggacacgaccttactactgctgcgaatctgcaat 300  
|||||  
DB 320 TCAGTGAGCAGCGCTGACCTGAGACGCGCCACATCTACTACTGTGCAAGCAATATTAAT 379  
QY 301 ggtgacagtgcttccttctggtgagctactgagacccaaggaactcctactcagcgtctc 360  
|||||  
DB 380 CGTTATCCCTTCTTGATATGATAGATGCTCTGGGGCCAGGAGACTCCAGGTCTACCGTCCACC 439  
QY 361 tca 363  
|||||  
DB 440 TCA 442

RESULT 6  
BE589545 505 bp mRNA linear EST 28-AUG-2000  
LOCUS BE589545  
DEFINITION 195790 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE589545  
VERSION BE589545.1 GI:9842584  
KEYWORDS EST.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

cow.  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 505)  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and  
Wells, K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross-match with the -minscore 18 and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCAGTCACGACG  
Plate: 122 row: F column: 3  
Seq primer: ATTTAGTGACCTATAC.  
Location/Qualifiers  
1..505  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 111 a 149 c 138 g 107 t  
ORIGIN

Query Match 66.0%; Score 239.6; DB 10; Length 505;  
Best Local Similarity 80.3%; Pred. No. 2.3e-55;  
Matches 294; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

QY 1 caggtgcagctcgaagagtcggagaccagctggtgaagccctcacagaccctctccctc 60  
|||||  
DB 80 CAGGTGCACCTCGCGAGTCGGGCCCCAGCCTGTGTAAAGCCCTCACAGACCTCTCCCTC 139  
61 acctgcagctctcgtgattcattcaaccaagatggtgtgagtggttcgcgagagct 120  
|||||  
DB 140 ACCTGCACGCTCTCTGGATTCTCATTTGACCACTATGCTGTAACTGTGGGTCGCCAGGCT 199  
QY 121 ccaggaagaagcgcttgagtgagctaggtggtggtccagtggtgacctaaagcctaacc 180  
|||||  
DB 200 CCGGGAAGGCGCTGGAGTGGATTGTGTAGTATGATTGTGTGAAGCAACATATTAAC 259  
QY 181 acagccctacagtcgccgaactcagcgtcaccaaggagacacctccaagaagccaattctccctg 240  
|||||  
DB 260 CCAGCCCTGAATAATCCGCGCTCAGACATCACCAAGGACCAAGCTCCAAGGCTCTCTG 319  
QY 241 tcaactgagcagctgagctactcagggacacgaccttactactgctgcgaatctgcaat 300  
|||||  
DB 320 TCAGTGAGCAGCGCTGACCTGAGACGCGCCACATCTACTACTGTGCAAGGATTTAAT 379  
QY 301 ggtgacagtc---gttcttctggtgagctactgagacccaaggaactcctactcagcgtc 357  
|||||  
DB 380 GGTGATGATTGGGATCTAATTAATGATGCTCTGGGGCCAGGAGACTCTGTGTCACCGTC 439  
QY 358 tctca 363  
|||||  
DB 440 TCCTCA 445



```

RESULT 7
LOCUS BE481532 456 bp mRNA linear EST 28-AUG-2000
DEFINITION 167023 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE481532
VERSION BE481532.1 GI:9601065
KEYWORDS EST.
SOURCE cDNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 456)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
JOURNAL Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt.-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCGCCAGTCACGACG
Plate: 20 row: J column: 7
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..456
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_1lb="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 101 a 129 c 125 g 101 t
ORIGIN
Query Match 65.1%; Score 236.2; DB 10; Length 456;
Best Local Similarity 83.5%; Pred. No. 1.8e-54;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 caagtcacactgcagagcgcgagccagcctgtgtgaagccctcacagaccctctcc 60
DB 80 CAGGTCACACTGGCGAGTCGGGCCCCAGGCTGTGAAGCCCTCACAGACCTCTCCCTC 139
QY 61 acctgcacggtctctgattctcatcaaccaagtatgtgttgattgtgtgcgcagcgt 120
DB 140 ACCTGACGCGTCTCTGATTCTCATTTGAGCAACTATGCTGTAGCTGGGTCGCCAGGCT 199
QY 121 ccaggaagagcgctgtgattggtcaggtaggtgtgtcagtggtgacttaacagcctaa 180
DB 200 CCAGGGAAGGCGCTGTGAGTCTCGGTAGTATTAACCAATGTGGAATAACAGGCTATTAAC 259
QY 181 acagccctacagtcgccgactcagcgttcacacagggacacctccaaagccaatctcc 240
DB 260 CCAGCCCTGAATAATCCCGGCTGACCATACCAAGCAACTCCAAAGCCCAAGTCTCTG 319
QY 241 tcactgacagcgtagactactagagacagcgccattactactgtgcgaatctgcaat 300
DB 320 TCAGTGACGAGCTGTGACCTGTAGGACAGCGCCACATACTACTGTGAAAAAAGTACTGCT 379
QY 301 ggtgacagtggttccctatggt 321

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DB 380 GGTCGACTGATTGATTATAG 400
RESULT 8
LOCUS BG692159 492 bp mRNA linear EST 02-MAY-2001
DEFINITION 341738 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BG692159
VERSION BG692159.1 GI:13933979
KEYWORDS EST.
SOURCE cDNA.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 492)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
JOURNAL Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt.-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCGCCAGTCACGACG
Plate: 41 row: F column: 19
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..492
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_1lb="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 102 a 152 c 134 g 104 t
ORIGIN
Query Match 64.8%; Score 235.4; DB 10; Length 492;
Best Local Similarity 80.2%; Pred. No. 3.2e-54;
Matches 291; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

QY 1 caagtcacactgcagagcgcgagccagcctgtgtgaagccctcacagaccctctcc 60
DB 85 CAGGTGAGAGTGGGGAGTAGAGGCCACAGCTGTGAAGCCCTCACAGACCTCTCCCTC 144
QY 61 acctgcacggtctctgattctcatcaaccaagtatgtgttgattgtgtgcgcagcgt 120
DB 145 ACCTGACGCGTCTCTGATTCTCATTTGAGCAACTATGCTGTAGCTGGGTCGCCAGGCT 204
QY 121 ccaggaagagcgctgtgattggtcaggtaggtgtgtcagtggtgacttaacagcctaa 180
DB 205 CCGGGGAAGGCGCTGTGAGTCTCGGTAGTATTAACCAATGTGGAATAACAGGCTATTAAC 264
QY 181 acagccctacagtcgccgactcagcgttcacacagggacacctccaaagccaatctcc 240
DB 265 CCAGCCCTGAATAATCCCGGCTGACCATACCAAGCAACTCCAAAGCCCAAGTCTCTG 324
QY 241 tcactgacagcgtagactactagagacagcgccattactactgtgcgaatctgcaat 300
DB 325 TCAGTGACGAGCTGTGACCTGTAGGACAGCGCCACATACTACTGTGAAAAAAGTACTGCT 384

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OY	301	ggtacagctgtccctcattggttgcagctactcggagcccgagacccactcactacacgtctcc	360
Db	385	GGTATATATTTATTTATTAAGC-----AGCTGGGGCCACAGACACTCTGTCACCGCTTCC	438
OY	361	tca 363	
Db	439	TCA 441	
RESULT 9			
LOCUS	BE846118	583 bp	linear EST 25-SEP-2000
DEFINITION	232255 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION	BE846118		
VERSION	BE846118.1	GI:10282942	
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
	1 (bases 1 to 583)		
REFERENCE	Sonstegard,T.S., Cepuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.		
AUTHORS	Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library		
TITLE	Unpublished (2000)		
JOURNAL	Contact: Sonstegard TS		
COMMENT	USA, ARS, Beltsville Agricultural Research Center		
	Bldg. 200 Rm 2A, Beltsville, MD 20705, USA		
	Tel.: 301 504 8416		
	Fax: 301 504 8414		
	Email: tads@ps1.barc.usda.gov		
	Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -mismc 18 and -mismatch 12 options.		
	PCR primers		
	FORWARD: AGGAAACAGCTATGACCAT		
	BACKWARD: GTTTCCAGTCACGACG		
	Plate: 112 row: P column: 20		
	Seq primer: ATTAGGTGACACTATAG.		
FEATURES	Location/Qualifiers		
source	1..583		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/clone_lib="BARC 5BOV"		
	/tissue_type="pooled"		
	/lab_host="DH10B"		
	/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."		
BASE COUNT	117 a	186 c	161 g 119 t
ORIGIN			
Query Match	64.8%;	Score 235.4;	DB 10; Length 583;
Best Local Similarity	80.2%;	Pred. No. 3.4e-54;	
Matches 291; Conservative	0;	Mismatches 66;	Indels 6; Gaps 1;
OY	1	caggtgcagctgcagagagctcggaaccagcctgltgaagcctcacaagacctctccctc	60
Db	79	CAGGTGAGCTGTCGGGAGTCTGCATTGTGACGACTATGCTGTAGCGCTGGCTCCGACGCTC	138
OY	61	acctgcaggtctctcggtattctatcaaccagaatagtggtgtagtgtggtccgcaggtc	120
Db	139	ACCTGCAGCGCTCTGGATTCTCATTTGAGCGACATATGCTGTAGCGCTGGCTCCGACGCT	198
OY	121	ccaggaagagcagcttgagtgcttagtggtgtgtccagctggtgtcactaagacctataac	180
Db	199	CCGGGGAAGCGCCCTGAGTGGT	258

QY	181	acagccctcagagctccagctcagctcagagacacacctcagaagacattctctc	240
Db	259	CCAGCCCTCGGAATATCCCGCTCAGCATCACCAAGACAACTCAAGACCAAGTCTCTG	318
QY	241	tcactgagcagctgactactgagacagcgccattactactcgtgcgaaatctgcaat	300
Db	319	TCAGTGAGCACCGTGACACCTCGAGGACACGGCCACATCTACTGTGCMAAGCTATTACT	378
QY	301	ggtacagctgtctcttaagtgttgactactcagggagccagagctcctactacgcttc	360
Db	379	GGTTATTATTATTATTATG-----AGCTGGGGCCAAAGACTCTGCTACCGTCTCC	432
QY	361	tca	363
Db	433	TCA	435
RESULT	10	BE485461	496 bp
LOCUS		172501 BARC 5BOV Bos taurus CDNA 5', mRNA sequence.	EST 28-AUG-2000
DEFINITION		BE485461	
ACCESSION		BE485461.1	GI:9604994
VERSION		EST.	
KEYWORDS		cow.	
ORGANISM		Bos taurus	
SOURCE		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	
REFERENCE		1 (bases 1 to 496)	
AUTHORS		Sonstegard,T.S., Capucio,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.	
TITLE		Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Sonstegard TS	
		USA, ARS, Beltsville Agricultural Research Center	
		Bldg. 200 Rm 2A, Beltsville, MD 20705, USA	
		Tel: 301 504 8416	
		Fax: 301 504 8414	
		Email: tads@psi.barc.usda.gov	
		Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.	
		PCR primers	
		FORWARD: AGGAACAGCTATGACCAT	
		BACKWARD: GTTTCCAGTCACGACG	
		Plate: 133 row: J column: 4	
		Seq primer: ATTAGGAGACATATAG.	
FEATURES		Location/Qualifiers	
SOURCE		1..496	
		/organism="Bos taurus"	
		/db_xref="taxon:9913"	
		/clone_lib="BARC 5BOV"	
		/tissue_type="pooled"	
		/lab_host="DH10B"	
		/note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."	
BASE COUNT		108 a	151 c
ORIGIN		138 g	99 t
Query Match		64.3%;	Score 233.4; DB 10; Length 496;
Best Local Similarity		79.6%;	Prod. No. 1.1e-53;
Matches 289; Conservative		0; Mismatches 71; Indels 3; Gaps 1;	
QY	1	caggtgcagctgcgaggaattcgagaccagcctcgtgtgaagcctcacaagacctcctc	60
Db	78	CAGGTGCAGCTGCGGGAATCGGCGCCACGCTGTGGAAGCCCTCAGACACCTGTGCTCC	137
QY	61	actgcagcgtctctcgtatctcattcaacaagatagtgttaagtttggtccgcagcgt	120

```

/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_id="BARC_5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

```

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease

Email: [cas@psi.barc.usda.gov](mailto:cas@psi.barc.usda.gov)  
Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCCACTCAGCAGG

Plate: 26 row: 6 column: 1

Seq primer: ATTGAGCAGACTATAG.  
Location/Qualifiers  
1..518

FEATURES

source

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease

BASE COUNT 109 a 150 c 149 g 110 t  
ORIGIN

Query Match 64.2%; Score 233; DB 10; Length 518;

Best Local Similarity 82.9%; Pred. No. 1.5e-53;  
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 caagtcagctcagagagtcggagccagcctgtggaagccctcaagaccctctccctc 60  
DB 97 CAGGTGACGTGCGCGAGTGGGCCCCAGCCTGGTGAAGCCTCAGACGCTCTCCCTC 156  
QY 61 acctgcagctctcttgatctcaatcaaccaagtaagtgttagttggtccgcagagct 120  
DB 157 ACCTGACGCGTCTGTGATTCTCATTTGACAGCATCTGTAAGCTGATCCGCGACAGCT 216  
QY 121 ccaggaaagcgcttgagtgagtgagtggtgtgtccagtggtgacctaaagcctataac 180  
DB 217 CCAGGGAAGGCGCTGGAGTCCCTGGGTATACACAGTGTGGAAACACAGGCTATTAAC 276  
QY 181 acagccctacagtcgccagctcagcgtctcaccagggacacacctcaagagcgaattctccctg 240  
DB 277 CCAGCCTGAATCCCGGCTCAGCATATCCAGAGACAATCCAGAGCCAAAGTCTCGCTG 336  
QY 241 tcactgagcagcgtgactactgagggacagcgccattactactctgtgcgaatctgtcaat 300  
DB 337 TCAGTGAGCAGCGCTGACCTGACCTGAGAGACGCGCACATACACTGTGCCAAAAGTTCTTAT 396  
QY 301 ggtgacagtgctctctatagt 321  
DB 397 GGTGGTGTGGCATAGTGTGT 417

## RESULT 13

BE482206 476 bp mRNA linear EST 28-AUG-2000  
LOCUS BE482206  
DEFINITION 167909 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE482206  
VERSION BE482206.1 GI:9601739  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 476)  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and  
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL 9land cDNA library  
COMMENT Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@lpsl.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGACGACGACG  
Plate: 22 row: 0 column: 5  
Seq primer: ATTTAGTGACACTATAG.

FEATURES  
Location/Qualifiers  
1..476

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 98 a 134 c 143 g 101 t  
ORIGIN

Query Match 64.0%; Score 232.2; DB 10; Length 476;  
Best Local Similarity 80.1%; Pred. No. 2.4e-53;  
Matches 305; Conservative 0; Mismatches 58; Indels 18; Gaps 2;

QY 1 caagtcagctcagagagtcggagccagcctgtggaagccctcaagaccctctccctc 60  
DB 13 CAGGTGACGTGCGCGAGTGGGCCCCAGCCTGGTGAAGCCTCAGACGCTCTCCCTC 72  
QY 61 acctgcagctctcttgatctcaatcaaccaagtaagtgttagttggtccgcagagct 120  
DB 73 ACCTGACGCGTCTGTGATTCTCATTTGACAGCATATGCTATAGACTGGTCCGCGACAGCT 132  
QY 121 ccaggaaagcgcttgagtgagtgagtggtgtgtccagtggtgacctaaagcctataac 180  
DB 133 CCAGGGAAGGCGCTGGAGTCCCTGGGTATTAAGTATGCTGGAACACAGCCTATTAAT 192  
QY 181 acagccctacagtcgccagctcagcgtctcaccagggacacacctcaagagcgaattctccctg 240  
DB 193 CCAGCCTGAATCCCGGCTCAGCATATCCAGAGACAATCCAGAGCCAAAGTCTCTCTG 252  
QY 241 tcactgagcagcgtgactactgagggacagcgccattactactctgtgcgaatctgtcaat 291  
DB 253 TCAGTGAGCAGCGCTGACCTGACCTGAGAGACGCGCACATACACTGTGCCAAAAGTGTGT 312  
QY 292 -----tcgtcaatggtgacagtggtctctatagt---tggactactgagccagga 342  
DB 313 GGTGGTATGTTGTGTGTGACGGTGTGATTATGATTAGCTCATGCTGGGGCAAGGA 372  
QY 343 ctccctacacagctctcccta 363  
DB 373 CTCCTGGTCAACGCTCTCTCA 393

## RESULT 14

BE589492 488 bp mRNA linear EST 28-AUG-2000  
LOCUS BE589492  
DEFINITION 195687 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE589492  
VERSION BE589492.1 GI:9842531  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 488)  
Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and  
Wells, K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL 9land cDNA library  
COMMENT Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@lpsl.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGACGACGACG  
Plate: 122 row: A column: 21  
Seq primer: ATTTAGTGACACTATAG.

# FEATURES

Location/Qualifiers  
1. 488

source  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPOT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 104 a 149 c 129 g 106 t

ORIGIN

Query Match 63.8%; Score 231.8; DB 10; Length 488;  
Best Local Similarity 77.4%; Pred. No. 3.1e-53;  
Matches 281; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1 caggtgacgtcagagagtcggagccagcctgtgtgaagccctcacagaccctctccctc 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 85 CAGGTGACGTCGGGGAGTCGGGCCCGCAGCTGTGTAAGCCCTCACAGACCTCTCCCTC 144  
QY 61 acctgacaggtctctggtatctcaataccaaglatgtgtgtgtgtgtgtgtgtgtgt 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 145 ACCTGACGCT 204  
QY 121 ccaggaagagcgtctgagtgctagtgctagtgctagtgctagtgctagtgctagtgct 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 205 CCAGGGAAGCGCTGAGTGGCTGACATACATTAACGATGATGAATACATTTCTTAAC 264  
QY 181 acagccctacagtcctcagctacagctacagctacagctacagctacagctacagct 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 265 CCAGCCCTGAATCCCGGCTCACATCACCAGAGACAACTCCAAAGCCAAAGTCTCTG 324  
QY 241 tcaatgacagcgtctgactactgagagacagcgcaattactactgtgtgcaatctgtcaat 300  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 325 GAAGTGTGACCTGTGACCTGTGAGACACGCGCACGACTACTGTGCAAAATGACTTGT 384  
QY 301 ggtgaagagtgctctatagtgctgactactgagccagagctcctacacagctctcc 360  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 385 AATTTTGGTTGTGACTTAACATTTGATGCTCTGGGCCCAAGACTCTGTACCGTCTGC 444  
QY 361 tca 363  
|||  
Db 445 TCA 447

RESULT 15  
BE478595 511 bp mRNA linear EST 28-AUG-2000

LOCUS BE478595 162919 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION BE478595  
ACCESSION BE478595.1 GI:9598128

VERSION  
KEYWORDS  
SOURCE

ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 511)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL 91and cDNA library  
COMMENT Unpublished (2000)

USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416  
Fax: 301 504 8414

Email: tadelpsl.barc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

PCR Primers  
FORWARD: AGGAACACAGCTATGACCAT  
BACKWARD: GTTTCCAGTCACGACG

Plate: 21 row: 0 column: 7  
Seq primer: ATTTAGGTGACACTATAG.

## FEATURES

source  
Location/Qualifiers  
1. 511

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPOT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 110 a 158 c 137 g 106 t

ORIGIN

Query Match 63.8%; Score 231.6; DB 10; Length 511;  
Best Local Similarity 79.0%; Pred. No. 3.5e-53;  
Matches 289; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 1 caggtgacgtcagagagtcggagccagcctgtgtgaagccctcacagaccctctccctc 60  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 80 CAGGTGACGTCGGGGAGTCGGGCCCGCAGCTGTGTAAGCCCTCACAGACCTCTCCCTC 139  
QY 61 acctgacaggtctctggtatctcaataccaaglatgtgtgtgtgtgtgtgtgtgtgt 120  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 140 ACCTGACGCT 199  
QY 121 ccaggaagagcgtctgagtgctagtgctagtgctagtgctagtgctagtgctagtgct 180  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 200 CCAGGGAAGCGCTGAGTGGCTGACATACATTAACGATGATGAATACATTTCTTAAC 259  
QY 181 acagccctacagtcctcagctacagctacagctacagctacagctacagctacagct 240  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 260 TCAGCCCTGAATCCCGGCTCACATCACCAGAGACAACTCCAAAGCCAAAGTCTCTG 319  
QY 241 tcaatgacagcgtctgactactgagagacagcgcaattactactgtgtgcaatctgtcaat 297  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 320 TCAGTACACGATTAACACCTGAGACACGCGCACATCTACTGTGCAAAAAGTCTTAT 379  
QY 298 aatgtgacagtgctctatagtgctgactactgagccagagctcctactacacgctc 357  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 380 AATTGGGCTACTGTTTAAATACGCTGATGCTTGGGCCAAGACATCTGTCAACCGTC 439  
QY 358 tctctca 363  
|||||  
Db 440 TCCTCA 445

Search completed: August 11, 2002, 21:30:32  
Job time: 6283 sec

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KW gene therapy; retrovirus; vector; pLNC-2e12h1g61CD58cPI; ss.  
 XX Synthetic.  
 OS  
 PN WO9720048-A2.  
 XX  
 PD 05-JUN-1997.  
 XX  
 XX 27-NOV-1996; 96WO-US19051.  
 PE  
 XX 30-NOV-1995; 95US-0007755.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Fell P, Hayden M, Ledbetter JA, Mittler R, Winberg G;  
 PI  
 DR WPI; 1997-310604/28.  
 XX  
 XX Modified sfv molecule for mediating adhesion between cells -  
 PT contains antibody binding site and transmembrane domain of receptor,  
 PT useful for enhancing immune responses to disease  
 XX  
 XX  
 PS Example 2: Fig 11A-B; 69pp: English.  
 XX  
 CC A nucleic acid sequence (AA769217) is provided of a modified sfv  
 CC encoded by retrovirus vector pLNC-2e12h1g61CD58cPI. This comprises  
 CC a fusion between hybridoma 2E12 sfv (see also AA769218), human IgG1  
 CC Fc portion (see also AA769219) and the transmembrane domain from the  
 CC CD8 glyco-phosphoinositol (GPI) anchor (see also AA769221) in vector  
 CC pLNC. This is an example of novel sfv molecules modified by  
 CC connecting a transmembrane domain of a cell surface receptor to the  
 CC antigen binding site of the molecule. This creates artificial  
 CC ligands that stimulate adhesion between cells and enhance co-  
 CC stimulatory activity during an immune response against disease.  
 CC Such vectors can be used for gene therapy of e.g. cancer.  
 XX  
 XX Sequence 1510 BP; 381 A; 422 C; 394 G; 313 T; 0 other;  
 XX

Query Match	Similarity	57.9%	Score 210;	DB 18;	Length 1510;
Best Local	Similarity	73.8%	Fred. No. 2.9e-52;		
Matches	267;	Conservative	0;	Mismatches	95;
				Indels	0;
				Gaps	0.
Qy	1	cagggtgcagctcgaagatcggagaccagccctggtggaagccctccacagacccttcctcc	60		
Db	380	cagggtgcagctcgaagagagatcagagacctggctctggtcggcgccctccacagagctctgctccatc	439		
Qy	61	acctgcacggtctctcgtatcttcataaaccaagatagtgtgtatggttgcgtccagagct	120		
Db	440	acatgcaccgctctcaggtcttcataaaccgctatgtgttaacatgggttcgcagcct	499		
Qy	121	ccaggaagaagcgcttgatgtgctgaagtgtgtctgcacagtgtgtgcactaacagacctataac	180		
Db	500	ccaggaagaaggtctctgaaatgctggtcgtggaatgatatagttggtatcgtgaagccacataataat	559		
Qy	181	acagccctcacagctcccgagctcagcgctccacccagagagaccctcccaagaccatcttcctcg	240		
Db	560	tcagctctccaaatccagagctgagctctaccacaaagagacaactccaagaagccaagtcttctcta	619		
Qy	241	tcactgcagacgctgtactactgagagacacagcgccatcttaactactgtggtgcgaactgtlcaat	300		
Db	620	aaaatgacaacgctctgcaactgatgacacagccagatatactactgtgcagagatgttat	679		
Qy	301	ggtgcacagtgtctccttaagtgttggaactactggaagcccgagagctcctactacacggtctcc	360		
Db	680	agtaactctcatatactagttaagtactactgtgggtccaagaaacctccagtacacgctctcc	739		
Qy	361	tc 362			
Db	740	tc 741			

AA69216	
ID	AA69216 standard; DNA; 1528 BP.
XX	
AC	AA69216;
XX	
DT	19-AUG-1997 (first entry)
XX	
DE	Retrovirus vector pLNC-2ei2h1g1b7-1Tm encoding modified sfv.
XX	
KW	Modified sfv; cell adhesion; artificial ligand; tumour; cancer;
KM	gene therapy; retrovirus; vector; pLNC-2ei2h1g1b7-1Tm; ss.
XX	
OS	Synthetic.
XX	
PN	W09720048-A2.
XX	
PD	05-JUN-1997.
XX	
PF	27-NOV-1996; 96WO-US19051.
XX	
PR	30-NOV-1995; 95US-0007755.
XX	
PA	(BRIM ) BRISTOL-MYERS SQUIBB CO.
XX	
PI	Fell P, Hayden M, Ledbetter JA, Mittler R, Winberg G;
XX	
DR	WPI; 1997-310604/28.
XX	
PT	Modified sfv molecule for mediating adhesion between cells -
PT	contains antibody binding site and transmembrane domain of receptor,
XX	useful for enhancing immune responses to disease
PS	Example 1: Fig 10A-B; 69pp; English.
XX	
CC	A nucleic acid sequence (AA69216) is provided of a modified sfv
CC	encoded by retrovirus vector pLNC-2ei2h1g1b7-1Tm. This comprises
CC	a fusion between hydridoma 2E12 sfv (see also AA69218), human IgG1
CC	Fc portion (see also AA69219) and the transmembrane domain from
CC	human B7-1 (CD80) (see also AA69220) in vector pLNC. This is an
CC	example of novel sfv molecules that are modified by connecting a
CC	transmembrane domain of a cell surface receptor to the antigen
CC	binding site of the molecule. This creates artificial ligands that
CC	stimulate adhesion between cells and enhance co-stimulatory
CC	activity during an immune response against disease. The vectors
CC	can be used for gene therapy of e.g. cancer.
XX	
SO	Sequence 1528 BP; 380 A; 434 C; 399 G; 315 T; 0 other;

[illegible]

QY	61	atgtgacggtctcttgatcttcctaaacaaagtatggtttagttggtccgacaggtc	12
Db	80	accgcacagctctcgtgttccctaaactagctatggttgcacctcgtgttcgcagctc	13
QY	121	ccaggaagaagcggtttagtgcgtatggtgtgtgtccagttggtgtacataagaactaaac	18
Db	140	ccaggaagaaggtctgagtggtgtggtgagtgatgtggtatgtgaataagaacacagactaant	19
QY	181	acagccctacagtcctccgactacagctcaccacagggacacctccaagagcaactctccctg	24
Db	200	tccagctctccaatcccgactagcatctcagcaagagcaactcccaagagcgaagtttctcta	25
QY	241	tcactatgcagcggtgactactagaagacagccattactactctgtgcaaatctgtcaat	30
Db	260	aaatgacacgctctgcaaacctgtagcaacagccacgaactactactctgtgccaaaggaatcccc	31
QY	301	ggtgacagtggttctctatgttcttgactactcggagcccggaactctctaccacgcgtccc	36
Db	320	tactatagagattactatgtctatgtgactactcgtgggccaagggaccacaggtccacgtctcc	37
QY	361	tca tca tca	363
Db	380	tca tca	382
RESULT	6		
AAAT77852			
ID	AAAT77852	standard; cDNA; 420 BP.	
XX	AAAT77852;		
DT	03-NOV-1997	(first entry)	
DE	Murine anti-human class II monoclonal antibody 44H104 HL chain cDNA.		
XX			
KW	Antibody; heavy chain; variable region; hybridoma cell line 44H104;		
KM	immune response; enhance; stimulate; vaccine; immunodiagnosis;		
KW	antigen delivery; ss.		
XX			
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..420	
FT		/*tag= a	
FT		/note= "Encodes 44H104 heavy chain variable region,	
FT		including secretion signal; termination	
FT		codon not given	
XX	WO9640941-A1.		
XX			
XX	19-DEC-1996.		
XX			
XX	07-JUN-1996;	96WO-CA00400.	
XX			
XX	07-JUN-1995;	95US-0483576.	
XX			
XX	(CONN-) CONNAUGHT LAB LTD.		
XX			
XX	Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;		
XX			
DR	WPI; 1997-077271/07.		
DR	P-Psdb; AAW22538.		
XX			
PT	Recombinant conjugate antibody mol., modified for delivering an		
PT	antigen - elicits enhanced immune response without the use of		
PT	adjuvant to generate antibodies which are useful in vaccines or		
PT	immuno:diagnosis		
PS	Example 1; Fig 1B; 64pp; English.		
CC	Novel recombinant conjugate antibody molecules comprise a monoclonal		
CC	antibody specific for a surface structure of antigen presenting		



XX	AAQI1845 standard; DNA; 363 BP.
XX	
AC	AAQI1845;
XX	
DT	31-JUL-1991 (first entry)
XX	
DE	Anti-placental alkaline phosphatase VH gene.
XX	
KW	Placental alkaline phosphatase; antibody; cancer; heavy chain;
KM	PLAP; CDR; ss.
XX	
OS	Mus musculus.
XX	
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	91..105
FT	/tag= a
FT	/label= CDRI
FT	148..195
FT	/tag= b
FT	/label= CDR2
FT	misc_feature
FT	292..330
FT	/tag= c
FT	/label= CDR3
XX	
PN	EP429242-A.
XX	
PD	29-MAY-1991.
XX	
PF	14-NOV-1990; 90EP-0312407.
XX	
PR	07-SEP-1990; 90GB-0019552.
PR	17-NOV-1989; 89GB-0026045.
XX	
PA	(UNIL ) UNILEVER PLC.
XX	
PI	Verhoeven ME;
XX	
DR	WPI; 1991-157662/22.
XX	P-PDSB; AARI1984.
XX	
PT	Synthetic specific binder for human placental alkaline
PT	phosphatase - for treating and diagnosing cancers e.g. breast,
PT	ovarian and colon cancers and pleural effusions
XX	
PS	Disclosure; Fig 1; 26pp; English.
XX	
XX	The murine anti-PLAP VH gene contains 3 CDRs which are used to reshape
CC	the human anti-PLAP VH gene (AAQI1847). The murine anti-PLAP VH gene
CC	(AAQI1846) CDRs were used to reshape the human anti-PLAP Vκ
CC	(AAQI1848). The specific binder for human PLAP contains at least
CC	one of the former 3 CDRs and/or at least one of the latter CDRs.
CC	The produced antibodies are more readily tolerated when administered
CC	to a human patient. Antibody reagents can be used to identify, e.g.
CC	by serum testing or imaging, and/or to treat PLAP-producing cancers.
CC	Such cancers can occur as, e.g. breast cancer, ovarian cancer and
CC	colon cancer or can manifest themselves as liquids such as pleural
CC	effusions.
XX	
XQ	Sequence 363 BP; 98 A; 94 C; 94 G; 77 T; 0 other;

Accession	Sequence	Length
Oy	ccaggaaagcgccttgatgctgctatgctgctgctgctccagctgctgctactaacagcctataac	160
Db	ccaggaaagcgccttgatgctgctatgctgctgctgctccagctgctgctactaacagcctataac	160
Oy	121 ccaggaaagcgccttgatgctgctatgctgctgctgctccagctgctgctactaacagcctataac	160
Db	121 ccaggaaagcgccttgatgctgctatgctgctgctgctccagctgctgctactaacagcctataac	160
Oy	181 acagccctcaacagctcccgactagctgctccagcgggacacctccagagccaatctccctg	240
Db	181 tcagcttcacatactccagactgagctgacatcaacagataatactccagagccaaagtcttctta	240
Oy	241 tcactgagcagcgtgactactcgtgagacacgagccattactactgctcgaaatctgccaat	300
Db	241 aaactcgaacacagctctgcaaacactgtagacacagccacgatactactctgccaaccccactac	300
Oy	301 ggtgcagcagctgctccattaggttttgacaaactggagccaggaaccccaaccacgctcttc	360
Db	301 ggtgcagcagctgctggtgggctatggaataactcgtggttcaagaaacctcaagtcacccgtcttc	360
Oy	361 tca 363	360
Db	361 tca 363	360

## RESULT 9

ID AAT40806 standard; cDNA to mRNA; 414 BP.

AC AAT40806;

DT 10-FEB-1997 (first entry)

DE Mab 10.1 heavy chain, directed against type II phospholipase A2.

KW Monoclonal antibody; phospholipase; myocardial infarction;  
 KW pancreatitis; cerebral infarction; acute kidney failure; colitis;  
 KW chronic rheumatism; adult respiratory distress syndrome;  
 KW cardiac shock; treatment; preclinical testing; disease; hybridoma;  
 KW ss.

05 Mus musculus.

FH	Key	Location/Qualifiers
----	-----	---------------------

$$\frac{F_T}{\star taq} = a$$

PN WO9620959-A1.

PD 11-JUL-1996.

PF 27-DEC-1995; 95WO-JP02714.

PR 29-DEC-1994; 94JP-0340006.

PA (YAMA ) YAMANOUCHI PHARM CO LTD.

PI Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;

DR WPI; 1996-333946/33.

XX

PT for treatment of myocardial and cerebral infarction

PS Example 6; Figure 14; 69pp; Japanese.

Monoclonal antibodies which inhibit type II phospholipase A2 are

infarction, acute kidney failure, chronic rheumatism, cardiac shock,

antibodies were generated by immunising Balb/c mice with recombinant

cc human c-type II phosphodiesterase  $\alpha 2$ . Spleen cells from mice were fused with mouse myeloma P3U1 (P3x63A $\alpha$ 8.11) and the hybridomas

CC Active clones were isolated including 12H5, 1.4 and 10.1. These



```
XX FH Key Location/Qualifiers
FT FT misc-feature 1..714
FT FT /tag- a
FT FT /note- "encodes single chain Fv fragment of
FT FT misc-feature 715..738
FT FT /tag- b
FT FT /note- "linker sequence"
FT FT misc-feature 739..0
FT FT /tag- c
FT FT /note- "encodes streptavidin"
XX XX WO9734634-A1.
XX PD 25-SEP-1997.
XX PF 20-MAR-1997; 97WO-0504427.
XX PR 20-MAR-1996; 96US-0013703.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PI Cheung NV, Guo H, Larson SM, Rivlin K, Sadelain M;
XX DR WPI; 1997-479996/44.
XX PT Recombinant single chain anti-disialoganglioside GD2 antibody -
XX PT useful to detect tumour cells expressing GD2 and to target
XX PT therapeutic agents, e.g. toxins, to such cells
XX PS Disclosure; Page 13; 31pp; English.
XX CC The present sequence encodes a recombinant single chain peptide,
XX CC 366-scFv-streptavidin. The peptide is an antibody construct comprising
XX CC the variable regions of the heavy and light chains of an antibody against
XX CC disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs
XX CC in many tumours types including neuroblastoma, osteosarcomas and other
XX CC soft tissue sarcomas, medulloblastomas, high grade astrocytomas,
XX CC melanomas and small cell lung cancer. The peptide can be detectably
XX CC labelled, preferably with 99m-Tc, for tissue imaging of cells expressing
XX CC GD2. It can also be used to target delivery of a therapeutic or
XX CC pre-therapeutic agent, such as a toxin, streptavidin (e.g. present
XX CC sequence) or a pro-drug converting enzyme, to cells expressing GD2. The
XX CC peptide may further comprise CD8 to facilitate the formation of
XX CC GD2-targeted lymphocytes. T cells containing the peptide can also be used
XX CC to target GD2-producing tumour cells.
XX SO Sequence 1173 BP; 270 A; 334 C; 340 G; 229 T; 0 other;
Query Match 51.6%; Score 187.4; DB 18; Length 1173;
Best Local Similarity 71.9%; Pred. No. 1.3e-45;
Matches 261; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 1 caggtgagctgcagagctgcggaccagcctgtggaagccctcaagacccttcctc 60
DB 1111111111111111111111111111111111111111111111111111111
DB 358 caggtgagctgcagagctgcggaccagcctgtggaagccctcaagacccttcctc 417
QY 61 accgcagctctcctgattcctcaatcaagatagtggttagttggtgcgcagagct 120
DB 1111111111111111111111111111111111111111111111111111111
QY 418 acttgacactgtctctggtttctcaatcaatatagtgttacactgtgttcgcagact 477
DB 478 ccaggaagaggtctcgagtgctgagatataatgagctgtgtggaagcacacaattataat 537
QY 181 acagcctacagtcgcagctcagctgcacagaggaacacctcaagagcaatttcctc 240
DB 1111111111111111111111111111111111111111111111111111111
DB 538 tcgctcttattgtccagctgagcatcagacagcaactcaagagcaagtttctta 597
QY 241 tcactgagcagcgtgactactgagacagcatttactactgttggaattcgtcaat 300
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DB 598 aaaaatgaacagctctgaacatgacacagccatgactactgtccagtcggyggagt 657
QY 301 ggtgacagctgtctcctactggttggaactactgagcccaagactcctcaaccgtctcc 360
DB 1111111111111111111111111111111111111111111111111111111
DB 658 aactaagg-----catgcttggaactactggtggtcaagaaacctcaagcagctctcc 711
QY 361 tca 363
DB 712 tca 714
RESULT 12
AAZ31382
ID AAZ31382 standard; DNA; 351 BP.
XX AC AAZ31382;
XX DT 07-FEB-2000 (first entry)
XX DE MMASWS1H M. musculus A.SW mRNA for ASWS1 antibody heavy chain.
XX KW Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;
XX KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
XX KW tumor-associated antigen; ss.
XX OS Mus sp.
XX PN US5977316-A.
XX PD 02-NOV-1999.
XX PF 16-JAN-1996; 96US-0591196.
XX PR 17-JAN-1995; 95US-0372676.
XX PA (KENT ) UNIV KENTUCKY.
XX PI Foon KA, Chatterjee SK, Chatterjee M;
XX DR WPI; 1999-619711/53.
XX PT Monoclonal antibody 1A7 which elicits an anti-GD2 immunological
XX PT response, useful for the development of products for the detection and
XX PT treatment of cancers -
XX PS Disclosure; Fig 13B; 74pp; English.
XX CC The invention provides a monoclonal antibody (Mab) designated 1A7, which
XX CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
XX CC humans. Mab 1A7 has defined light and heavy chain variable region
XX CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an
XX CC anti-GD2 immune response. The polypeptides can also be used for
XX CC detecting or purifying anti-GD2 antibody. The products can be used for
XX CC treating GD2-associated diseases, e.g. melanoma, neuroblastoma, glioma,
XX CC soft tissue carcinoma, and small cell carcinoma. They can be used for
XX CC palliating the disease or for reducing the risk of recurrence. Sequences
XX CC AAZ31373-90 represent sequences that closely matched Mab 1A7 heavy chain
XX CC variable region encoding sequence.
XX SO Sequence 351 BP; 95 A; 87 C; 88 G; 80 T; 1 other;
Query Match 51.5%; Score 187; DB 20; Length 351;
Best Local Similarity 72.2%; Pred. No. 1.2e-45;
Matches 260; Conservative 0; Mismatches 91; Indels 9; Gaps 1;
QY 1 caggtgagctgcagagctgcggaccagcctgtggaagccctcaagacccttcctc 60
DB 1111111111111111111111111111111111111111111111111111111
DB 1 caggtgagctgcagagctgcggaccagcctgtggaagccctcaagacccttcctc 60
QY 61 accgcagctctcctgattcctcaatcaagatagtggttagttggtgcgcagagct 120
DB 1111111111111111111111111111111111111111111111111111111
DB 61 acatgcactgtctctggttctcattatccagatagatgtaacactgtgttcgcagact 120
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Dd		121	ccaggaaagggccttgcagttggtctgggaatgatatgggtgggtggaaaacacagactataat	180
Oy		181	aagaccctacagctccgcactcagctcagctcaccaagacaccccacaagaagccaattctccctg	240
Dd		181	tcaagctccaatctccacactcagactgtagcatcagaagacaacccccacaagaagccaagtttcccta	240
Oy		241	.tcaactagcagcgtgactactcaggaagacagggccattactactgtgtgcgaatctgtcaat	300
Dd		241	aaaaatgaacagctctgcacaactgcatagcacacgccactgactactcgtgtccagagatggttac	300
Oy		301	ggtgacagctgtctcttatgttgttgactactcggagcccaagactcctactaccgctctcc	360
Dd		301	tacgac-----tatgctatgactactcgtgggttaagaaactcgaaccctgcacgctctcc	351
RESULT_13				
ID	AAT43413	standard; cDNA to mRNA; 357 BP.		
XX	AAT43413;			
AC				
XX				
DT	17-FEB-1997	(first entry)		
XX				
DE	Xenograft antibody IH2IH7 heavy chain variable region CDNA.			
XX				
KW	Xenograft rejection; xenotransplantation; organ transplant;			
RN	animal model; pig; monoclonal antibody; IH2IH7; ds.			
XX				
OS	Rattus sp.			
FT	Key	Location/Qualifiers		
FT	CDS	1..357		
FT		/tag= a		
FT		/product= Immunoglobulin variable region		
FT		/strand.name= Ig heavy chain variable region		
FT		/label= VH Region		
FT		/note= "IH2IH7 heavy chain variable region"		
FT	misc_RNA	1..291		
FT		/tag= b		
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FT		/label= VH Segment		
FT		/note= "variable segment of IH2IH7 heavy chain variable region"		
FT	misc_RNA	292..312		
FT		/tag= c		
FT		/strand.name= Ig Heavy chain diversity segment		
FT		/label= D-Segment		
FT		/note= "diversity segment of IH2IH7 heavy chain variable region"		
FT	misc_RNA	313..357		
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FT		/strand.name= Ig heavy chain joining segment		
FT		/label= JH-Segment		
FT		/note= "joining segment of IH2IH7 heavy chain variable region"		
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FT		/tag= e		
FT		/strand.name= Framework region 1		
FT		/label= FR-1		
FT		/note= "framework region 1 of IH2IH7 heavy chain variable region"		
FT	misc_RNA	91..105		
FT		/tag= f		
FT		/strand.name= CDR-1		
FT		/label= CDR-1		
FT		/note= "complementarity determining region 1 of IH2IH7 heavy chain variable region"		
FT	misc_RNA	106..151		
FT		/tag= g		
FT		/strand.name= Framework region 2		

FT	/label= FR-2
FT	/note= "framework region 2 of IH2IH7 heavy chain
FT	variable region"
FT	152..198
FT	/*tag= h
FT	/standard_name= CDR-2
FT	/label= CDR-2
FT	/note= "complementarity determining region 2 of
FT	IH2IH7 heavy chain variable region"
FT	199..291
FT	/*tag= i
FT	/standard_name= Framework region 3
FT	/label= FR-3
FT	/note= "framework region 3 of IH2IH7 heavy chain
FT	variable region"
FT	292..324
FT	/*tag= j
FT	/standard_name= CDR-3
FT	/label= CDR-3
FT	/note= "complementarity determining region 3 of
FT	IH2IH7 heavy chain variable region"
FT	325..357
FT	/*tag= k
FT	/standard_name= Framework region 4
FT	/label= FR-4
FT	/note= "framework region 4 of IH2IH7 heavy chain
FT	variable region"
PN	WO9636358-A1.
XX	21-NOV-1996.
XX	14-MAY-1996;
PF	96WO-US06804.
XX	15-MAY-1995;
PR	95US-0440621.
XX	(CEDA-) CEDARS SINAI MEDICAL CENT.
PA	Cramer DV, Makowka L, Wu G;
PI	WPI; 1997-011852/01.
XX	P-PSDB; AAM06204.
DR	Inhibiting xenograft rejection by modifying antigen expression of
PT	the graft - prevents binding of anti-donor antibody and prolongs
PT	graft survival
XX	Claim 7; page 113-114; 135pp; English.
PS	A cDNA clone (AAI43413) codes for the variable heavy chain segment
CC	(AAM06204) of the LEW rat anti-porcine xenograft monoclonal antibody
CC	IH2IH7. It was obt'd from a IH2IH7 heavy chain cDNA library by
CC	phage display and PCR amplification, and can be used to produce
CC	recombinant IH2IH7 antibody fragments, e.g. Fab'12 and Fab'
CC	These block binding of preformed anti-donor xenograft antibodies in
CC	a recipient animal serum to antigen expressed by endothelial cells
CC	of the xenograft, i.e. they inhibit antibody-mediated rejection,
CC	thereby prolonging the survival of the pig xenograft in the
CC	recipient.
SO	Sequence 357 BP; 89 A; 97 C; 92 G; 79 T; 0 other;
Query Match	51.3%; Score 186.4; DB 18; Length 357;
Best Local Similarity	71.8%; Pred. No. 1.8e-45;
Matches 260; Conservative	0; Mismatches 96; Indels 6; Gaps 1;
OY	2 aggtcagcttcgaggatcgccacgcagcttgtaagccccaagaccctctcccta 61
Db	
	2 aggtcaagctgcagcggcttccaggaacctggcctggttcagcaccctcacagaccctgctctca 61
OY	62 ccgtcagcgttccttgatctcatataacaagaatagtgtcttagttgggtccgccaggtctc 121





FT /note= "no STOP codon given"

XX MO9636361-A1.

PN 21-NOV-1996.

XX 16-MAY-1996; 96MO-US07113.

XX 18-MAY-1995; 95US-0443540.

XX (UNMI ) UNIV MICHIGAN.

XX Glick GD, Swanson PC;

XX WPI: 1997-011854/01.

DR P-PSDB: AAM07437.

XX Anti-DNA antibody which specifically binds DNA hairpin - useful to  
PT develop prods. for diagnosis and treatment of disorders, e.g.  
PT glomerulonephritis or systemic lupus erythematosus

XX Example; Fig 9; 102pp; English.

XX The present sequence encodes the heavy chain variable region of the  
CC group 11f8 putative consensus anti-DNA monoclonal antibody (Mab),  
CC which has a high affinity for single stranded DNA, low or no  
CC affinity for double stranded DNA and specifically binds a DNA  
CC hairpin. The Mab can be used to diagnose disorders associated with the  
CC pathological complexation of DNA, e.g. inflammatory  
CC glomerulonephritis and systemic lupus erythematosus. It can also be  
CC used to generate reagents to screen for pharmaceutical agents, and  
CC treat and/or prevent an above disorder.  
CC The sequence was derived by aligning homologous anti-DNA Mab cDNA,  
CC whose sequences have been published, as well as several Mab of  
CC other specificities obtained from a database search.

XX Sequence 369 BP; 93 A; 95 C; 92 G; 89 T; 0 other;

Query Match 51.0%; Score 185; DB 18; Length 369;

Best Local Similarity 72.6%; Pred. No. 4.6e-45;  
Matches 268; Conservative 0; Mismatches 95; Indels 6; Gaps 2;

QY 1 caggctcagctgagagagtcgagccagcctgtgtaagccctcacagaccctccctc 60  
DB 1 caggctcagctgagagagtcgagccagcctgtgtaagccctcacagaccctccctc 60  
QY 61 acctgcacggtctctgtatctcattaaaccaagtatgtgttagttgcgcagcgt 120  
DB 61 acctgcacggtctctgtatctcattaaaccaagtatgtgttagttgcgcagcgt 120  
QY 121 ccaggaaaggcgttgtagtgctagtggtgt--gtccagtggtgacctaagcctat 177  
DB 121 ccaggaaaggcgttgtagtgctagtggtgt--gtccagtggtgacctaagcctat 177  
QY 178 aacacagccctacagtcaccagtcacagtcacagtcacagtcacagtcacagtcac 237  
DB 181 aatcgcgtctcatgtccagcagtcagtcagtcagtcagtcagtcagtcagtcagtc 240  
QY 238 ctgtcacctgagcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 297  
DB 241 ttaaaatgacacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
QY 298 ---aatggtgacagtcgttcttctttagtttagtactgagccagagtcctactacc 354  
DB 301 ccttaatggtgacagtcgttcttctttagtttagtactgagtcagtcagtcagtcagtc 360  
QY 355 gtctcctca 363  
DB 361 gtctcctca 369

Search completed: August 11, 2002, 22:10:19  
Job time: 7699 sec

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GenCore version 4.5  
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# OM nucleic - nucleic search, using sw model

Run on: August 11, 2002, 19:46:55 ; Search time 1984.69 Seconds  
(without alignments)  
3827.466 Million cell updates/sec

Title: US-09-786-015-1  
Perfect score: 363  
Sequence: 1 cagctgcagctgcagagctc.....tccactcaccgtctccca 363

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:\*

- 1: gb\_da:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_da:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vl:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	265.4	73.1	456	4	OAVRA17IG	249176 O.aries MRN
2	254.2	70.0	456	4	OAVRA10IG	249175 O.aries MRN
3	251	69.1	426	4	OAVRA11IG	249192 O.aries MRN
4	251	69.1	450	4	OAVR66IG	249172 O.aries MRN
5	251	69.1	456	4	OAVRA15IG	249159 O.aries MRN
6	251	69.1	458	4	OAVRA41IG	249170 O.aries MRN
7	249.4	68.7	369	4	AF172680	AF172680 Ovis arle
8	249.2	68.7	461	4	OAVRA4IG	249156 O.aries MRN
9	247.6	68.2	366	4	AF172674	AF172674 Ovis arle
10	247	68.0	449	4	OAVR21IG	249166 O.aries MRN
11	246.6	67.9	447	4	OAVRB1IG	249171 O.aries MRN
12	246.2	67.8	458	4	OAVRA12IG	249164 O.aries MRN
13	246	67.8	366	4	AF172667	AF172667 Ovis arle
14	246	67.8	366	4	AF172670	AF172670 Ovis arle
15	246	67.8	458	4	OAVR11IG	249158 O.aries MRN
16	244.8	67.4	429	4	OAVRB7IG	249193 O.aries MRN
17	244.6	67.4	422	4	OAVR20IG	249165 O.aries MRN
18	243	66.9	363	4	AF172668	249160 O.aries MRN
19	242.8	66.9	430	4	OAVG10IG	249180 O.aries MRN
20	242.8	66.9	453	4	OAVR31IG	U55202 Bos taurus
21	242.2	66.7	462	4	BTU55202	U55202 Bos taurus
22	241.8	66.6	469	4	OAVR15IG	AF172666 Ovis arle
23	240.2	66.2	357	4	AF172666	AF172666 Ovis arle
24	239.8	66.1	360	4	AF172671	AF172671 Ovis arle
25	239.4	66.0	351	4	AF172659	AF172659 Ovis arle
26	238.6	65.7	452	4	OAVRB14IG	249173 O.aries MRN
27	238	65.6	1581	4	BTIG61HCX	X62916 B. taurus MR
28	235.4	64.8	450	4	OAVR10IG	249168 O.aries MRN
29	235	64.7	360	4	AF172665	AF172665 Ovis arle
30	235	64.7	457	4	OAVR18IG	249167 O.aries MRN
31	235	64.7	736	4	OAV7AIG	249186 O.aries MRN
32	235	64.7	847	4	OAV1B1G	249188 O.aries MRN
33	234.2	64.5	406	4	OAVGVRB3	250036 O.aries MRN
34	234	64.5	475	4	OAVR5IG	249178 O.aries MRN
35	233.4	64.3	455	4	OAVRB2IG	249174 O.aries MRN
36	233.4	64.3	464	4	OAVRA19IG	249177 O.aries MRN
37	233.4	64.3	739	4	OAVSAIG	249187 O.aries MRN
38	233.4	64.3	1923	4	OAVGMU	X59994 O.aries MRN
39	231.8	63.9	360	4	AF172664	AF172664 Ovis arle
40	231.8	63.9	430	4	OAVGE70IG	249181 O.aries MRN
41	231.8	63.9	455	4	OAVR16IG	249163 O.aries MRN
42	231.8	63.9	507	4	TTR320196	AJ320196 Tursteps
43	231.6	63.8	366	4	AF172660	AF172660 Ovis arle
44	231	63.6	351	4	AF097208	AF097208 Bos tauru
45	231	63.6	408	4	BTU49782	U49782 Bos taurus

## ALIGNMENTS

RESULT 1

OAVRA17IG 456 bp MRNA linear MAM 04-FEB-1998

LOCUS O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRA17).

ACCESSION Z49176

VERSION Z49176.1 GI:794120

KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.

SOURCE Sheep.

ORGANISM Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

REFERENCE 1 (bases 1 to 456)

AUTHORS Dufour,V.

TITLE Direct Submission

JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022

2 (bases 1 to 456)

REFERENCE Dufour,V., Malinge,S. and Nau,F.

AUTHORS The sheep Ig variable region repertoire consists of a single VH family

JOURNAL		J Immunol . 156 (6), 2163-2170 (1996)	
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		/issue_type="spleen"	
		/rearranged	
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		37..>456	/gene="VH"
CDS		/codon_start=1	
		/product="VH region precursor"	
		/protein_id="CA899045.1"	
		/db_xref="GI:794121"	
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		385..456	
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BASE COUNT	88 a 144 c 127 g 97 t		
ORIGIN			
Query Match	73.1%; Score 265.4; DB 4; Length 456;		
Best Local Similarity	83.2%; Pred. No. 1.1e-69;		
Matches 302; Conservative	0; Mismatches 61; Indels 0; Gaps 0;		
OY	1 caggtgcagctgcaggaatcggaaccagcctgtgtgaagccctacacagacctctccctc 60		
DB	94 CAGGTGCGGCTCCAGAGAGCGGGACCCAGCCTGTGTGAAGCCCTCCACAGACCTCTCCCTC 153		
OY	61 acctgcagctctcgcgaattcattcaaccagaatagtatgtttagttagttggtcccgagcgt 120		
DB	154 ACCTCACAGGCTCTCGAATTCATTAAACAGCAATGCTGTAGACTGGGTCCGCGAGGCT 213		
OY	121 ccaggaagaagcgcttgatgctaggtgtgtgttcacagtgtgtgcaatacagcctataac 180		
DB	214 CCAGGAAAGGTCCCGGAGTGGCTGTGTGTGTATMAACAGTAGAGGAAGCACAATACTATAAC 273		
OY	181 acagccctacagctccgcgactcagcgtccacagcaggaacacactccaaagaccaattctccctg 240		
DB	274 CCGGCTCTGAATATCCCGGCGACATCATACAGAGGAGCGCTCCAAAGACCAAGTCTCCCTG 333		
OY	241 tcaactgaagcagctgtactactgtgagacacgcccattactactgtgcgaatctgtcaat 300		
DB	334 TCACTAGACAGCGGTGACAACTGAGACCGCGCGTGTACTACTGTGCCGCACTTGATAT 393		
OY	301 gttgcagtggttccctatagtgttgcactactgtgaagcccaagagcctctactacgcgtccc 360		
DB	394 AGTGGCTGTGCTTGTGTTCATGACACTACTGTGGGCCCCAGGACTCTGGTACCGGTCC 453		
OY	361 tca 363		
DB	454 TCA 456		
RESULT	2		
LOCUS	OAVRA10IG	456 bp	linear
DEFINITION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRA10).		
ACCESSION	Z49175		
VERSION	Z49175.1		
KEYWORDS	GI:794118		
	diversity region; immunoglobulin; immunoglobulin heavy chain;		

SOURCE	joining region; variable region.
ORGANISM	sheep.
Ovis aries	
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;	
Bovidae; Caprinae; Ovis.	
1 (bases 1 to 456)	
Dufour.V.	
Direct Submission	
Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA	
1172, IBM/GT, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022	
2 (bases 1 to 456)	
Dufour.V., Malinge,S. and Nau,F.	
The sheep Ig variable region repertoire consists of a single VH	
family	
J. Immunol. 156 (6), 2163-2170 (1996)	
96310953	
JOURNAL MEDLINE FEATURES	
source	Location/Qualifiers
	1..456
	/organism="Ovis aries"
	/db_xref="taxon:9940"
	/clone="VRA10"
	/tissue_type="spleen"
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	/gene="VH"
CDS	37..>A56
	/gene="VH"
	/codon_start=1
	/product="VH region precursor"
	/protein_id="CA8904.1"
	/db_xref="GI:794119"
	/translation="MNPMLTLFLYSLAPRGVLSOVLEESGPSLVRPSQTLISLTCTVS
	GFSITSNNGVROAPGKALEWGVDIRAGSKSEYSPALKRRLSTIRDTSKSYSLSS
	SVTEEDPAVYYCARDQPSSEGFDDYMGRLATYS"
sig_peptide	37..87
	/gene="VH"
V_region	88..456
	/gene="VH"
	/product="VH region"
D_segment	385..456
	/gene="VH"
	/note="D-JH region"
BASE COUNT	100 a 136 c 125 g 95 t
ORIGIN	
Query Match	70.0%; Score 254.2; DB 4; Length 456;
Best Local Similarity	81.3%; Pred. No. 2.7e-66;
Matches 295; Conservative 0; Mismatches 68; Indels 0; Gaps 0;	
Qy	1 caagtcacgctgcgaagatcggaaaccagcctgtgtgaagccctcaacacctctccctc 60       Db
94 CAGTGCGACACTGGAGAGCGGGACCACGCTGTGAAGCCCTCAGACCCCTCTCCCTC 153 	
Qy	61 acctcgacggtcttcggattctcatlaaccaagtatggttgttagttggtccgacagct 120       Db
154 ACCTCACAGGCTCTGGATTCTCATTAACCAACAATAATGTAAGCTGGGTCGCCAGGCT 213 	
Qy	121 ccaggaaaagcgcttgatgtgtcgtgtgtgtgtcctcagttggtgtgcataacagccataac 180       Db
214 CCAGGAAGAAGGCCTGTGAGTGGTGTGTGACATATATGTCTGTGTGAGAAAGATATATAGC 273 	
Qy	181 acagccctaagtcgccgaactcagctcaacccaggagacacctccaagaagcaattctccctg 240       Db
274 CGCGCCCTGAAACCCCCGCTCAGCATCTCACAGAGGACACCTCCAAAGCCAAAGTCTCCCTG 333 	
Qy	241 tcaatgagagaggttactactatgagacaacggcattactactactgtggaaatctgtcaat 300 
Db	334 TCACTAGAGAGCGGTGACACTGAGAACACGGCCGTGTACTGTGTGCAAGAGATCAGCCT 393 
Qy	301 ggtagcacgtgttccctatgattgtgtaactactggaaccaggaactcctaactacacgtctcc 360 

Db 394 AGTAGGCGCTGTTGGTATACGACTACTGGGCCACGACTACTGTCACCGTCTCC 453  
QY 361 tca 363  
Db 454 TCA 456

RESULT 3  
LOCUS OAVRB11G 426 bp mRNA linear MAM 04-FEB-1998  
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region  
(clone VRB11).  
ACCESSION 249192  
VERSION 249192.1 GI:794127  
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;  
joining region; variable region.  
SOURCE sheep.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
REFERENCE 1 (bases 1 to 426)  
AUTHORS Dufour,V.  
TITLE Direct Submission  
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA  
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022  
REFERENCE 2 (bases 1 to 426)  
AUTHORS Dufour,V. and Nau,F.  
TITLE Sheep immunoglobulin mu heavy chain variable region sequence  
JOURNAL Unpublished  
FEATURES  
source Location/Qualifiers  
1..426  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
/clone="VRB11"  
/tissue\_type="spleen"  
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1..426  
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1..>426  
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/codon\_start=1  
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/protein\_id="CAA89051.1"  
/db\_xref="GI:794128"  
/translation="MNPLWTLFLVLSAPRGVLSQVRLQSGSLVKSSQTLSTCTVS  
GFSLSNAVGMVROAPGKAPENVAGIHNHSGISGYNPALSKRLSITRDTSKQVSLSL  
SVTADTPMYTCARDYSGCGRSVACIDYWGPLIVTSS"  
1..51  
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52..426  
/gene="VH"  
/product="VH region"  
349..426  
/gene="VH"  
/note="D-JH region"  
BASE COUNT 87 a 128 c 116 g 95 t  
ORIGIN

Query Match 69.1%; Score 251; DB 4; Length 426;  
Best Local Similarity 82.1%; Pred. No. 2, 6e-65;  
Matches 303; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 1 caggtcagctgcaggaagtcggagccagcctgtgaagccctcaagaccctctcctc 60  
Db 58 CAGGTGCGGCTGCAGAGTCGGAGCCAGCGCTGTGAAGCTCTCACAGACCTCTCCCTC 117  
QY 61 acctgcagcgtctctgattctcatcaacaagaatgagttgagttgggtccgacaggtc 120  
Db 118 ACCTGCAGCGTCTCTGATTCTCATTAACCAAGCAATGCTTAGAGCTGGGTCGCCAGGCT 177  
QY 121 ccaggaagcgcttgagtgctaggtgtgtgtccagtgagtgactaagacgtataac 180

Db 178 CCAGAAAGCGCCGCGAGTGGTGTGATACATATAGTGAAGTATAGGCTATTAAC 237  
QY 181 acagccctacagtcctccgaccctcagctcagcagggacccctccaaagacatctccctg 240  
Db 238 CCAGCCCTTAAGTCCCGCTCCAGCATCACCGAGCACCTCCCAAGAGTCAAGTCTCCCTG 297  
QY 241 tcaactgcagcagctgactacagggagacagggccattactacactgtgagc-----aaatc 294  
Db 298 TCACTGACAGCGGTGACAGCTGAGGACACGCCCATGTACTACTGTGCAGAGATTATAGT 357  
QY 295 gtcactgtgacagctgtctcttactgtgttgactactgcagcagccagagctcctacc 354  
Db 358 GGATGTGCTGCTGATGCTGTGCTGTATGAGTACTAGGGGCCAGAGATCTCGTCAACC 417  
QY 355 gtctctctca 363  
Db 418 GTCTCTCTCA 426

RESULT 4  
LOCUS OAVRB6IG 450 bp mRNA linear MAM 04-FEB-1998  
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region  
(clone VRB6).  
ACCESSION 249172  
VERSION 249172.1 GI:794137  
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;  
joining region; variable region.  
SOURCE sheep.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
REFERENCE 1 (bases 1 to 450)  
AUTHORS Dufour,V.  
TITLE Direct Submission  
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA  
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022  
REFERENCE 2 (bases 1 to 450)  
AUTHORS Dufour,V., Malinge,S. and Nau,F.  
TITLE The sheep Ig variable region repertoire consists of a single VH  
family  
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)  
MEDLINE 96310953  
FEATURES  
source Location/Qualifiers  
1..450  
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/tissue\_type="spleen"  
/rearranged  
31..450  
/gene="VH"  
31..>450  
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/protein\_id="CAA89041.1"  
/db\_xref="GI:794138"  
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/note="D-JH region"  
BASE COUNT 99 a 139 c 116 g 96 t  
ORIGIN

Query Match	69.1%;	Score 251;	DB 4;	Length 450;
Best Local Similarity	80.7%;	Pred. NO. 2.6e-65;		
Matches 293; Conservative	0;	Mismatches 70;	Indels 0;	Gaps 0;

QY	1	caggctgagctgcaagagtcgagaccgaagccctggtgaaagccctcaagaacctctccctc	60
Db	88	CAGGTGCAAGCTCAGGAAGTGGGCTCCAGACCTGGTGAAGACCTTCACAGACCTTCTCCCTC	147
QY	61	acctgcacgctctcgtgattctcattaaaccaagatagtgtgtagtgttggtccgcagagct	120
Db	148	ACCTCAGAGGCTCTGTGATTTCTCAATTAAGACAGCATGTGTTAACTGGGTCCGCAGGCT	207
QY	121	ccagaagaagcgcttgatgtgcttaaggctgctgtgtccagtggtgcactaagacctataac	180
Db	208	CCAGGGAAGGCACTGGAGTGGGTTGGTACAGATTGATTAAGGTGGATAACTACATATAAC	267
QY	181	acagaccctacagctccgcagctcagctcaacgaagagacactccaaagaagcaattctcccg	240
Db	268	GCGGCCCTTGAAATCCCGGCTCAGCAATCACACAGGAGACCTCCAAAGAGCCCAAGTCTCCCTA	327
QY	241	tcaactgagcagcgctactactctgagacacagcgcatcttactctgtgcaaatctgcaat	300
Db	328	TCACGTGACAGGGTACACAACAGAGACACAGCGCGGTGTACTGGAGTGCACAACCTGCGCTTTAT	387
QY	301	ggtgacagtgctccttaagtgttgactactactgagcccaagacctcctactacacgcttc	360
Db	388	AGGCTTGTTCATATCAATATGAGACACGCCCTACGTGAGCCCGAGCACTCTGTGTACACGGTTCC	447
QY	361	tca 363	
Db	448	TCA 450	

RESULT	5
LOCUS	OAVRB151G
DEFINITION	OAVRB151G 456 bp mRNA linear MAM 04-FEB-1996
ACCESSION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRB15).
VERSION	249159
KEYWORDS	249159.1 GI:794131 diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region. sheep.
SOURCE	Ovis aries
ORGANISM	Euarchyotia; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Caprinae; Ovis.
REFERENCE	1 (bases 1 to 456) Dufour, V.
AUTHORS	Direct Submission
TITLE	Submitted (27-ARR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE	2 (bases 1 to 456) Dufour, V., Malinge, S. and Nau, F.
AUTHORS	The sheep Ig variable region repertoire consists of a single VH family
TITLE	J Immunol. 156 (6), 2163-2170 (1996)
JOURNAL	96310953
MEDLINE	
FEATURES	
SOURCE	Location/Qualifiers 1..456 /organism="Ovis aries" /db_xref="taxon:9940" /clone="VRB15" /tissue_type="spleen" /rearranged 37..456 /gene="VH" 37..>456 /gene="VH" /codon_start=1 /product="VH region precursor"

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/protein_id="CAAB9028.1"
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/translation="MNPIMTILFVLSARGVLSOVQOGSGPSLYKPSQILFLICTYS
GFSLISYAVNMVRQAPGKALEWGNILINDGFTYNNPALKSLISRDTSSQVSLSLSS
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37..87
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V_region
88..456
/gene="VH"
D_segment
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385..456
/gene="VH"
/note="D-JH region"
BASE COUNT 100 a 138 c 112 g 106 t
ORIGIN

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Query Match	69.1%	Score 251;	DB 4;	Length 456;
Best Local Similarity	80.7%	Pred. No. 2.6e-65;		
Matches 293; Conservative	0;	Mismatches 70;	Indels 0;	Gaps 0;

QY	1	cagggtcgaagctgcaggagatccggagaccacagccctggtgaaagccctcaacagacccttccttc	60
Db	94	CAGGTTTCAGCTTCAGAGGGTCGGAGCCACAGCTGTGTGAAGCCCTCACAGACCTCTTCTC	153
QY	61	acctcagcagctctcgtatctcattcaataacaaagatagtgtgtatgttggtccgcagagct	120
Db	154	ACCTCAGCAGGTCCTCGAGATTCATTAAACCACTATGCTGTAACTGGTCCGCCAGGCT	213
QY	121	ccaggaanaagcgcttgatgtagtgaagtgtgtgtgtccagtgatgtgcaatacagccataac	180
Db	214	CCAGGAAAGGCACTGGAGAGGGGTGTGTAACATTCTAAATGATGAGAAATACATATATATAT	273
QY	181	aagagccctacagctcccgactacagtcgtcaaccagggagacotccaagaagcaatcttcctgt	240
Db	274	CCGGCCCTGTAATCCCGGCTCAGCATCTTCCAGAGGACACCTCCAAAGCAAGCAATCTTCCCTG	333
QY	241	tcaactgagcagatgtactactatgagaacaagcgcatcttaactactgtgcgaatcttcaat	300
Db	334	TCACGTGAGCAGCGTTACAACTGAGACACAGCGCGGTGTACTACTGTGTCAAGAGGGGGTATT	393
QY	301	ggtgcagatgtctccttaagtgttgcactactagagcccaagacctcctactacacgcttcc	360
Db	394	TATTACTACTACTGTGACGTGTATCAACTACTGGGGCCAGACACTCCTGGTACACGCTTCC	453
QY	361	tca 363	
Db	454	TCA 456	

RESULT	6
LOCUS	OAVRA4IG
DEFINITION	OAVRA4IG 458 bp mRNA linear MAM 04-FEB-1998 (clone VRA4).
ACCESSION	Z49170
VERSION	Z49170.1 GI:794125
KEYWORDS	diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region. sheep.
SOURCE	Ovis aries
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis. 1 (bases 1 to 458) Dufour/V. Direct Submission Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022 2 (bases 1 to 458) Dufour,V., Mallinge,S. and Nau,F. The sheep Ig variable region repertoire consists of a single VH family
REFERENCE	
AUTHORS	
TITLE	

JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)  
MEDLINE 96310953  
FEATURES  
source Location/Qualifiers  
1..458  
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/rearranged  
39..458  
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GFLSTSNVHWROAPGKVPFWLGIATGSGTFYKPALMSRLSITRDSKSKQVLSLS  
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90..458  
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Best Local Similarity 80.7%; Pred. No. 2.6e-65;  
Matches 293; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
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DB 96 CAGGTGCGACTGCGAGAGTCGGAGCCAGCGCTGTGAAGCCCTCACAGACCCTCTCC 155  
QY 61 acctgacagctctctggtatctcattaaaccaagtagtggtgtgtgtgtgtgtgtgt 120  
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DB 156 ACCTGACAGCGTTCTGATTCTCATTAACCAAGCAATGCTGTACACATGGGTCGCCAGGCT 215  
QY 121 ccaggaaagcgctgtgagtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180  
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DB 216 CCGAGAAAGTGCAGAAATGCTGGTGTGATTCACACTGGTGGAGACACATTCATTAAG 275  
QY 181 acagccctacagtcaccagctcagcgttcacagaggaacctcacaagagccaattctcc 240  
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DB 276 CCGGCCCTAATGTCGGCGCTCACACATCACAGGACAGCTCCAAAGCCAGTCTCCCTG 335  
QY 241 tcactgacagcgtgtgactactgagagacagcgcaattactactgtgcgaaatctgtcaat 300  
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DB 336 TCACCTAGAGAGCTAACAAGTGAACGACGCGGTGTACTACTGTCAAGAAGATATTCAGT 395  
QY 301 ggtgacagtgcttctactatggttggactactgagcccaaggaacctactaccagctctcc 360  
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DB 396 GGTACTGTGAATGTCTGGGATATCGAAACCTGGGGCCCAAGACTCTGTGTCACGTTCTC 455  
QY 361 tca 363  
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DB 456 TCA 458  
RESULT 7  
AF172680 369 bp mRNA linear MAM 01-SEP-1999  
LOCUS AF172680  
DEFINITION Ovis aries clone 146 immunoglobulin heavy chain precursor (IGHV)  
MRNA, partial cds.  
ACCESSION AF172680  
VERSION AF172680.1 GI:5815228  
KEYWORDS

SOURCE sheep.  
ORGANISM Ovis aries  
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.  
REFERENCE  
AUTHORS 1 (bases 1 to 369)  
TITLE White G.P., Meusen, E.N.T. and Newton, S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
nematode parasite Haemonchus contortus  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 369)  
AUTHORS White G.P., Meusen, E.N.T. and Newton, S.E.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Center  
for Animal Biotechnology, The University of Melbourne, Parkville,  
Melbourne, Victoria 3052, Australia  
FEATURES  
source Location/Qualifiers  
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contortus"  
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LEWGAIVYDGSASVYPAKSRVTRDRISKQVLSLSVTEDTAVVYVYCARDRSV  
YGHAYISIDYMWGPGLVTVSS"  
BASE COUNT 78 a 112 c 96 g 83 t  
ORIGIN  
Query Match 68.7%; Score 249.4; DB 4; Length 369;  
Best Local Similarity 81.8%; Pred. No. 7.9e-65;  
Matches 302; Conservative 0; Mismatches 61; Indels 6; Gaps 1;  
QY 1 cagggtcagctgcaggagtcggagaccagcctgtgtgaagccctcacagacccttcctc 60  
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DB 1 CAGGTGCAACTGCGAGAGTCGGAGCCAGCGCTGATGAAGCCCTCACAGACCCTCTCCCTC 60  
QY 61 acctgacagctctctggtatctcattaaaccaagtagtggtgtgtgtgtgtgtgtgtgtgtgtgt 120  
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DB 61 ACCTGCTCGGTCTGTGATTCTCATTAACCAAGCAATGCTGTGTAGTCGTGTCGCCAGGCT 120  
QY 121 ccaggaaagcgctgtgagtcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180  
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DB 121 CCGAGAAAGCTGAGAGTGGTGGTTCATTAATATGATGATGAAGTGCATCTTAATAC 180  
QY 181 acagccctacagtcaccagctcagcgttcacagaggaacctcacaagagccaattctcc 240  
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DB 181 CCGGCCCTGAATTCGGCGCTCACACATCACAGGACAGCTCCAAAGCCAGTCTCCCTG 240  
QY 241 tcactgacagcgtgtgactactgagagacagcgcaattactactactgtgcgaaatctgtcaat 300  
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DB 241 TCACCTAGAGAGCTAACAAGTGAACGACGCGGTGTACTACTGTCAAGAAGATATTCAGT 300  
QY 301 ggtgacagtgcttctactatggtt-----gactactgagcccaaggaacctactacc 354  
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DB 301 AGGTCTAATGTCATGCTTATCTGTCCATGCACTACTAGGGGCCAGAGACTCTGTGTCAC 360  
QY 355 gttctcctca 363  
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DB 361 GTCTCTCA 369

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RESULT      8
LOCUS       OAVR41G
DEFINITION  OAVR41G 461 bp mRNA linear MAM 04-FEB-1998
              (clone VR4).
ACCESSION   Z49156.1 GI:794113
VERSION     249156.1
KEYWORDS    diversity region; immunoglobulin; immunoglobulin heavy chain;
              joining region; variable region.
SOURCE      sheep.
ORGANISM   Ovis aries
REFERENCE   1 (bases 1 to 461)
AUTHORS     Dufour V.
TITLE       Direct Submission
JOURNAL     Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
              1177, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
REFERENCE   2 (bases 1 to 461)
AUTHORS     Dufour V., Malinge S. and Nau F.
TITLE       The sheep Ig variable region repertoire consists of a single VH
              family
JOURNAL     J. Immunol. 156 (6), 2163-2170 (1996)
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QY 1 caagtcacgtgcagagatcgagaccagcctgtgaagccctcacagacccttcctc 60
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DB 96 CAGGTGACAGTGCAGAGATCGGAGACCCCGCTGTGAGAGCCCTCAGACAGACCTCTCCCTC 155
QY 61 acctgcaggtctcttgatctcatlaaccaaglatgltagttggtcgcagagct 120
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DB 156 ACCTGCACGGTCTCTGATTCATTAAGCAGCAATTCTATTCTGGGTCGCCAGGCT 215
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DB 216 CCAAGAAAGGCACTGAGAGTGCGTTCATATTATTAAGAAAGAACACACCTATTAAC 275
QY 181 acagccttaagtcacgactcagcgtcacacaggaacacccccaagagccaattctccctg 240
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DB 276 CCGGCCCCGAATCCCGGATCAGCATACCGAGGACACCTCCAAAGCCAAAGTCTCCCTG 335
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DB 336 TCACTAGCAGCGCTGACAACTGAGACACGCGCATATCTACTGTGAAATATTCGAAT 355
QY 301 ggtgacagtggtctctatggttg---gactactgagaccagagactcctactacacgctc 357
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DB 396 GGTGAGCGTTTGTGATGATGATGAGGCGAGCTACTGAGGCGCCAGAGACTCTGTCGCTG 455
QY 358 tctctca 363
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DB 456 TCCTCA 461
RESULT      9
LOCUS       AF172674
DEFINITION  AF172674 366 bp mRNA linear MAM 01-SEP-1999
              Ovis aries clone 92 immunoglobulin heavy chain precursor (IGHV)
              mRNA, partial cds.
ACCESSION   AF172674
VERSION     AF172674.1 GI:5815217
KEYWORDS    nematode parasite Haemonchus contortus
SOURCE      sheep.
ORGANISM   Ovis aries
REFERENCE   1 (bases 1 to 366)
AUTHORS     White, G.P., Meusen, F.N.T. and Newton, S.E.
TITLE       A single-chain variable region immunoglobulin library from the
              abomasal lymph node of sheep infected with the gastrointestinal
              nematode parasite Haemonchus contortus
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 366)
AUTHORS     White, G.P., Meusen, F.N.T. and Newton, S.E.
TITLE       Direct Submission
JOURNAL     Submitted (26-JUL-1999) School of Veterinary Science, The Center
              for Animal Biotechnology, The University of Melbourne, Parkville,
              Melbourne, Victoria 3052, Australia
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BASE COUNT  80 a 111 c 97 g 78 t
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Best Local Similarity 81.7%; Pred. No. 2.8e-64;
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QY 1 caagtcacgtgcagagatcgagaccagcctgtgaagccctcacagacccttcctc 60
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DB 1 CAGGTGCACTGCAAGAGTGGGACCCAGCTGTGAAGCCCTCAGACAGACCTCTCCCTC 60
QY 61 acctgcaggtctcttgatctcatlaaccaaglatgltagttggtcgcagagct 120
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DB 61 ACCTGCACGGTCTCTGATTCATTAACCTAACAATGCTGTACACGGGTCGCCAGGCT 120
QY 121 ccaggaagagcgcttgatggtcagtggtgtgtccagtggtgcactaacgcctaac 180
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DB 121 CCAAGAAAGTGCCTGGAGTGCTTGGTAGATCAGCAGAGTGCTGAAGCACATCTATAAT 180
QY 181 acagccttaagtcacgactcagcgtcacacaggaacacccccaagagccaattctccctg 240
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Db	96	CAAGTCCGGCTCCAGAGATCCGGACCCAACTCGTGAACCTTCACAGACCCCTTCCTC	155
OY	61	acctgacagctctcgtatctcattcaataccaagiatgggtgtagtgggtccgcaagct	120
Db	156	ACCTGCACAGGTCCTCGGGCTTCATTAAACACACCTACAGTGAAGGCTGGGTCGGCAGGCT	215
OY	121	ccaggaagaagcgctgtagtggctaaagtgtgtgtgtcagtggtgcctaaacagccataac	180
Db	216	CCAGGAAGAAGCGCCTGAGTGGCTGTGTGTATGAAGAAATGATGATGTGCACAGCTATCAT	275
OY	181	acagccctcaacagctcccgactcagcgctcacacagagacacctcccaagagccaattccctg	240
Db	276	CCAGCCCTTAAGTCCCGGCTCAGCATCAACAGAGACACCTCCAAAGAGCAAGTCCCTG	335
OY	241	tcactgagcagcgctgactactcaggaagacagcgccattctactgtgcgaatctgcaat	300
Db	336	TCACGACAGCGGTGACAGATGAGGACACGGCAATGACTGTGTGTAAGAAAGTTTTC	395
OY	301	ggtagcagtgctctcattggtgtgacactcagcgagccagagacctcctaaccgctcc	360
Db	396	GGTGGAA-----AATACGTGGGGCTACTGTGGGCCACAGACCTCTGATCAGGCTCTCC	446
OY	361	tca	363
Db	447	TCA	449
RESULT	11		
OVERB1G			
LOCUS			
DEFINITION	O.aries mRNA for immunoglobulin mu heavy chain variable region (clone VRB1).	447 bp	linear
ACCESSION	Z49171		
VERSION	Z49171.1	GI:794133	
KEYWORDS	diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.		
SOURCE	sheep.		
ORGANISM	Ovis aries		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.		
REFERENCE	1 (bases 1 to 447)		
AUTHORS	Dufour V.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022		
REFERENCE	2 (bases 1 to 447)		
AUTHORS	Dufour V., Malinge S. and Nau F.		
TITLE	The sheep Ig variable region repertoire consists of a single VH family		
JOURNAL	J. Immunol.	156 (6),	2163-2170 (1996)
MEDLINE	96310953		
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	34..84		
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Best Local Similarity	82.1%;	Pred. No. 5,66-64;	
Matches 298;	Conservative 0;	Mismatches 59;	Indels 6; Gaps 1;
OY 1	caagtcagcctgcagagagtcggagaccagccctggtgtaagccctcacagaccctcctc 60		
Db 91	CAGGTGCGGCTGCAGAGATCGGAGCCGACCGCTGGTGAAGCCCTCAGACACCTTCCTC 150		
OY 61	acctgcagagctctcggattctcattaccagaatggtgtgtagtgtggtccgcaagct 120		
Db 151	ACCTGCAGGGTCTCTGGATTCATTAACCAAGCTATGGTGAAGCCTGGGTCGCGCAGGCT 210		
OY 121	ccaggaagagcagctgtaatgctaggtgtgtgtcctcagctgtgtgcactaacacataac 180		
Db 211	CCAGGAAGAAGCGGCTATGATGCTGCTGTGTATATGAGAGATGGAAGAACAACATATGAC 270		
OY 181	aacagccctacagtcctccgactcaagcgtcacccagagacacctccaaagaccattccctg 240		
Db 271	CCAGCCTTCAGTCCGCCGACTCAGCACTATGAGGACACCTCCAAAGAGCAGAGTCCCTTA 330		
OY 241	tcacctgagcagcgtgacctactcagagacacggccattactactctgtgcgaatctgcaat 300		
Db 331	TCACGTGACACAGGATGACAACTGATATATCGGCGGTGACTACTGT-----ACTGAATT 384		
OY 301	gctgacagctgtccctcattcgtgttcagactcagagaccccaagacactcactacacgtctcc 360		
Db 385	GCTTACTATGCGCAATTGTGAGATCTACTCTCTGCGGCCCGGAGACTCTCTGTGACCGCTTCC 444		
OY 361	tca 363		
Db 445	TCA 447		
RESULT 12			
OAVR12IG			
LOCUS	458 bp	mRNA	linear MAM 04-FEB-1998
DEFINITION	O. aries mRNA for immunoglobulin mu heavy chain variable region (clone VR12).		
ACCESSION	Z49164		
VERSION	249164.1		
KEYWORDS	GI:794093		
SOURCE	diversity region; immunoglobulin; immunoglobulin heavy chain; joining region; variable region. sheep.		
ORGANISM	Ovis aries		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.		
AUTHORS	1 (bases 1 to 458)		
TITLE	Dufour V.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022		
AUTHORS	2 (bases 1 to 458)		
TITLE	Dufour V., Malinge, S. and Nau, F.		
JOURNAL	The sheep Ig variable region repertoire consists of a single VH family		
MEDLINE	J. Immunol. 156 (6), 2163-2170 (1996)		
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Matches 290; Conservative % 0; Mismatches 73; Indels 0; Gaps 0;		
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QY	61	acctcacggtctctgatactcaatcaacaagaatagtgttagtttggtctgccagagct 120
Db	156	ACCTCAGAGGCTCTCGAATTCTCATTAACAACATAGTGTGCAGGCTGGGTGCCGAGGCT 215
QY	121	ccaagaaaagcgcttagtgagtgctagggtgtgtgtgtccagtgagtgtaactaacagcctataac 180
Db	216	CCAGGAAAGCGGCTTGAGATGCTGTGATACATACTAATGAGGGGGAACCTTTAAC 275
QY	181	acagccctaacagctcccagctacagctcaacggagaaacctcaagagcaattctccctg 240
Db	276	CAAGCCCTTAAGTCCCGGCTCAGCATTAACACAGGGACACTTCCAAGAGCCAGAGTCTCCCTT 335
QY	241	tcaactgaagcagcgttacactcagagagacacggccaatctactactgtgcgaatctgtcaat 300
Db	336	TCACTGAGACACGCGTGGCCAGTAGAGGATACGGCCGCTGTCACTTGTGTTCGTTTTGGTAGT 395
QY	301	ggtgacagtgttccttaatgtgtgttgactactcagagacactcctaactcactacacgctcc 360
Db	396	GGTGGCGGCGCTGTGATGGAGATCGACTACATACGAGGCCCCAGAGATCCTGTGCACCGTCTCC 455
QY	361	tca 363
Db	456	TCA 458
RESULT_13		
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DEFINITION	Ovis arles clone 47 immunoglobulin heavy chain precursor (IGHV)	
ACCESSION	AF172667	mRNA, partial cds.
VERSION	AF172667.1	GI:5815203
KEYWORDS		
SOURCE		
ORGANISM	Ovis arles	Sheep.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis. 1 (bases 1 to 366) White,G.P., Meusen,E.N.T. and Newton,S.E.	

ACCESSION	AF172670
VERSION	AF172670.1
KEYWORDS	GI:5815209
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ORGANISM	sheep. Ovis aries
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
AUTHORS	1 (bases 1 to 366)
TITLE	White, G.P., Meusen, E.N.T. and Newton, S.E. A single-chain variable region immunoglobulin library from the abomasal lymph node of sheep infected with the gastrointestinal nematode parasite Haemonchus contortus
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 366)
AUTHORS	White, G.P., Meusen, E.N.T. and Newton, S.E.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUL-1999) School of Veterinary Science, The Center for Animal Biotechnology, The University of Melbourne, Parkville, Melbourne, Victoria 3052, Australia
FEATURES	Location/Qualifiers
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CDS	1..366 /gene="IGHV" /note="IGHV" /codon_start=1 /product="immunoglobulin heavy chain precursor" /protein_id="AA52597.1" /db_xref="GI:5815210" /translation="OYOQESGPSLVKPSQTLSTCTVSGSLTNVAVGWROAPGRKAL LEWGAIVDSGNTDYNPALKRSRLGITRDTSTNQVSLSSVTTEDFVAVYCVRMVNDN TYGAVYIDVWMPGLLVYSS"
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61	acctgcacgctctcgatctcattcaataccaagatagtgtagtgggtccgcagcgt 120
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121	CCAGGAAGGCAATGGATGGGTGGTGCATATGAGATAGGAGGAATACAGACTATAC 180
181	acagccctcacagctccgcagctacgcgtccacgaagacacctccaagaagcaattccctg 240
181	ACAGCCCTCAAGATCCCGACTCGCATCAACAGGACACCTCCACAAACACAGGTCTCCTG 240
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301	ggtgaca---gtgttccttatggtttgtagactactggaagcccaagactctactcacggtc 357
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QY 358 tcctca 363  
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RESULT 15

OAVER11G 458 bp mRNA linear MM 04-FEB-1998  
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 (clone VR11)..  
 ACCESSION 249158  
 VERSION 249158.1 GI:794091  
 KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;  
 joining region; variable region.  
 SOURCE sheep.  
 ORGANISM Ovis aries  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 458)

REFERENCE  
 AUTHORS Dufour V.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA  
 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022  
 2 (bases 1 to 458)  
 REFERENCE Dufour V., Malinge S. and Nau F.  
 AUTHORS The sheep Ig variable region repertoire consists of a single VH  
 TITLE family  
 JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)  
 MEDLINE 96310953  
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QY 61 acctgacggctctctgattctcatlaaccaaglatggtttagttgggtccgcaagct 120  
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 Db 153 ACCTGACGGGTCTCTGATTCTCATTTAGTACAAATGCTGTAGAGCTGCGCAGGCT 212  
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QY 121 ccaggaagagcgtctgagtgctagtggtgtctccagtggtgcactaacacctataac 180  
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Db 213 CCAGAAAGACACTGAGTGGGTAGGGAATATATGAGTGAATGAGATACATATATAAC 272  
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QY 181 acagccctacagtcgccgactcagcgtcacccagggagacactccaagagccaatctccctg 240  
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Db 273 CCGGCCCTGAATCCCGGCTCAGCATCACAGGACCTCCAAAGCCAAAGTGTCCCTG 332  
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QY 241 tcactgacgcgtgactactgagagacacggtccattactactgtgcgaatctgcaat 300  
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Db 333 TCAGTACGAGCGGTATCATTTGACGACAGGCGCGTGTACTACTGTGCAGAGATGAGAT 392  
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QY 301 ggtgac---agtgctcctatggttggactactggaagccaggaactcctactacgctc 357  
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Db 393 AGTGGCTGAGACTTATGTGGAGGTATCGACTCTGGGCGCAGGACTCCTGTGTACCGTTC 452  
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About: Results were produced by the GenCore software, version 4.5  
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gb_estc2:BE8588530	+ 427.50	837.39	2.1e-37	581	BE8588530 195987 BARC SBOV Bos t
gb_estc2:BE8484553	+ 427.00	837.71	2.0e-37	498	BE8484553 171651 BARC SBOV Bos t
gb_estc2:BE8480749	+ 427.00	837.08	2.1e-37	515	BE8480749 165937 BARC SBOV Bos t
gb_estc2:BE8688447	+ 426.50	836.76	2.3e-37	513	BE8688447 336072 BARC SBOV Bos t
gb_estc2:BE8767159	+ 425.00	834.42	3.1e-37	484	BE8767159 160181 BARC SBOV Bos t
gb_estc2:BE8692179	+ 424.00	832.26	4.1e-37	492	BE8692179 341738 BARC SBOV Bos t
gb_estc2:BE846118	+ 424.00	830.41	5.2e-37	583	BE846118 232255 BARC SBOV Bos t
gb_estc2:BE8692167	+ 423.00	829.12	6.2e-37	547	BE8692167 342157 BARC SBOV Bos t
gb_estc2:BE8691073	+ 422.50	826.88	8.2e-37	613	BE8691073 340089 BARC SBOV Bos t
gb_estc2:BE8485514	+ 422.00	828.07	7.1e-37	502	BE8485514 173210 BARC SBOV Bos t
gb_estc2:BE8483181	+ 421.50	826.84	8.3e-37	513	BE8483181 165933 BARC SBOV Bos t
gb_estc2:BE8692735	+ 421.00	826.99	8.1e-37	462	BE8692735 342677 BARC SBOV Bos t
gb_est1:AV8668243	+ 421.00	824.99	1.0e-36	555	AV8668243 AV8667743 Bos taurus ovis
gb_estc2:BE8457585	+ 420.50	824.99	1.0e-36	507	BE8457585 232825 BARC SBOV Bos t
gb_estc2:BE8476654	+ 419.00	823.99	1.2e-36	637	BE8476654 176725 BARC SBOV Bos t
gb_estc2:BE8688665	+ 419.00	819.52	2.1e-36	509	BE8688665 336371 BARC SBOV Bos t
gb_estc2:BE8486006	+ 418.50	821.24	1.7e-36	497	BE8486006 173340 BARC SBOV Bos t
gb_estc2:BM106851	+ 417.50	818.70	2.4e-36	523	BM106851 510810 BARC SBOV Bos t
gb_estc2:BM086541	+ 417.00	817.64	2.7e-36	526	BM086541 498314 BARC SBOV Bos t
gb_estc2:BE8590022	+ 416.50	816.61	3.1e-36	528	BE8590022 196806 BARC SBOV Bos t
gb_estc2:BE8483736	+ 416.50	816.71	3.0e-36	573	BE8483736 170020 BARC SBOV Bos t
gb_estc2:BE8589795	+ 415.00	816.39	3.2e-36	410	BE8589795 196341 BARC SBOV Bos t
gb_estc2:BE8592569	+ 415.00	814.88	3.8e-36	471	BE8592569 342309 BARC SBOV Bos t
gb_estc2:BE8690115	+ 415.00	814.88	4.4e-36	516	BE8690115 338540 BARC SBOV Bos t
gb_estc2:BE8487460	+ 414.50	813.89	4.4e-36	501	BE8487460 176139 BARC SBOV Bos t
gb_estc2:BE8689490	+ 414.00	812.24	5.4e-36	470	BE8689490 337581 BARC SBOV Bos t

34 aIsETrpValArgGlnAlaProGlyLysAla

```

|||||
113 TAAAGTGGTCCGCGCAGCTCCAGGAGGCGTGGATGTCCTGGTGGT 162
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
163 ATAAGTATGATGGTGAAGACACAGCCTATATCCAGCCTGAAATCCCGGCT 212
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSerS 84
213 CACATCCACCAAGACCAACTCCAAAGACCAGTCTCTCTGCTCAGTGAAGA 262
84 eValThrThrGluAspThrAlaAlaLeuTyrCysAlaLysSerValAsn 100
263 GCGTGACAACTGAGACGCGCCACATCTACTGTGCGAAAAAAGTGGT 312
101 GlyAspSerValProTyrGly.....Le 108
313 GGTGGT.....TATGCTGTGGTGGAGGCGTGCCTATATGATATGCT 353
108 uAspTyrTrpSerProGlyLeuLeuLeuThrValSerSer 121
354 CGATGCTGGGCGCAAGACTCCTGCTGTCACCGTCTCCTCA 393
seq_name: gb_est2:BE846229

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seq_documentation_block:
LOCUS BE846229 579 bp mRNA linear EST 25-SEP-2000
DEFINITION 232099 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE846229
VERSION BE846229.1 GI:10283053
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 579)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGACGACGAG
Plate: 112 row: J column: 9
Seq primer: ATTATGCTGACACTATAG.

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## FEATURES

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source
1..579
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 108 a 171 c 166 g 134 t
ORIGIN

```

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alignment_scores:
Quality: 447.50 length: 134

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```

Ratio: 4.106 Gaps: 1
Percent Similarity: 81.343 Percent Identity: 68.657
align seg 1/1 to: BE846229 from: 1 to: 579

```

```

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnThr 17
64 CAGGTGACGCTGGGAGGTGGGCGCCAGCCTGTGTAAGCCCTCAGCAGAC 113
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
114 CCTCTCCCTCAGCTGACGCGTCTCTGATTCATTTGACGACGATATCTG 163
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnTrrPleuGlyGly 50
164 TAGGCTGGTCCGCGCAGCTCCGCGGAGGCGCTGGAGTGGTGGTGGT 213
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
214 ATAAGTATGATGGTGAAGACACAGCCTATATCCAGCCTGAAATCCCGGCT 263
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSerS 84
264 CAGATCCACCAAGACCAACTCCAAAGACCAGTCTCTCTGCTCAGTGAAGA 313
84 eValThrThrGluAspThrAlaAlaLeuTyrCysAlaLysSer..... 98
314 GCGTGACAACTGAGACGCGCCACATCTACTGTGCGAAAAAAGTGG 363
99 .....ValAsnGlyAspSerVal 104
364 GGTATTATGGTTATAGTCTTATAGTTGCTGTGATATGTTATAGTTA 413
104 lProTyrGlyLeuAspTyrTrpSerProGlyLeuLeuLeuThrValSerS 121
414 TGGTTACAGACTCGATCCTGCGGCGCAAGACATCTGTCACCGTCCCT 463
121 er 121
464 CA 465
seq_name: gb_est2:BE589545

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seq_documentation_block:
LOCUS BE589545 505 bp mRNA linear EST 28-AUG-2000
DEFINITION 195790 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589545
VERSION BE589545.1 GI:9842584
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 505)
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -minmatch 12 options.
PCR Primers

```

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FEATURES
source
1..505
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT 108 a 171 c 166 g 134 t
ORIGIN

```

```

alignment_scores:
Quality: 447.50 length: 134

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FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACGACGACGAC  
 Plate: 122 row: F column: 3  
 Seq primer: ATTAGTGACACTATAG.

FEATURES  
 source Location/Qualifiers

1..505  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC 5BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."

BASE COUNT 111 a 149 c 138 g 107 t  
 ORIGIN

## alignment\_scores:

Quality: 444.50 Length: 123  
 Ratio: 4.154 Gaps: 2  
 Percent Similarity: 86.992 Percent Identity: 73.984

## alignment\_block:

US-09-786-015-2 x BE589545 ..

Align seg 1/1 to: BE589545 from: 1 to: 505

```

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
80 CAGGTGACGTCGGCGGAGTCAGGCCAGCCTGTGTAAGACGCTACAGAC 129
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrpGly 34
|||||
130 CCTCTCCCTACCTGACGAGCTCTGTGATTTCTTGAAGACGATCTGTG 179
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
180 TAGACTGGTCGCCGACGCTCGGGGAAAGCGCTGGATGGATGGATG 229
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerAla 67
|||||
230 ATAGTGTGTGTAGAACACATCTACTATACCCAGCCCTAAATCCCGCT 279
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
280 CAGCATACCAAGACACACTCCAGAGCCAGACTCTCTGTGACGTAGACA 329
84 erValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
|||||
330 GCGTGACACTGAGACAGCGCCACATCTACTGTGCAAGGCTTATAT 379
101 GlysPseSer.....ValProTyrGlyLeuAspTyrTrpSerProGly 115
|||||
380 GGTGATGTGGGATCTACTATATGTT...GATGCTGGGGGCCAGGACT 426
115 uLeuLeuThrValSerSer 121
|||||
427 CTTGGTACCGCTCTCTCA 445
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seq\_name: gb\_est2:BE480296

seq\_documentation\_block:

LOCUS BE480296 514 bp mRNA linear EST 28-AUG-2000  
 DEFINITION 165337 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE480296  
 VERSION BE480296.1 GI:9599829

KEYWORDS EST.  
 SOURCE cow.

ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE  
 1 (bases 1 to 514)  
 AUTHORS  
 Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and  
 Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary

JOURNAL gland cDNA library  
 COMMENT Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2N, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414  
 Email: tads@lpsl.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross-match with the -minscore 18  
 and -mismatch 12 options.

PCR PRIMERS

FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACGACGACGAC  
 Plate: 16 row: D column: 1  
 Seq primer: ATTAGTGACACTATAG.

FEATURES  
 source Location/Qualifiers

1..514  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC 5BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"

/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."

BASE COUNT 103 a 161 c 137 g 113 t  
 ORIGIN

## alignment\_scores:

Quality: 441.50 Length: 128  
 Ratio: 4.088 Gaps: 2  
 Percent Similarity: 84.375 Percent Identity: 72.656

## alignment\_block:

US-09-786-015-2 x BE480296 ..

Align seg 1/1 to: BE480296 from: 1 to: 514

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
75 CAGGTGACGTCGGCGGAGTCAGGCCAGCCTGTGTAAGACGCTACAGAC 124
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrpGly 34
|||||
125 CCTCTCCCTACCTGACGAGCTCTGTGATTTCTTGAAGACGCTATCTG 174
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
175 TATCCTGGTCGCCGACGCTCCAGGAAAGCGCTGAGATCTTGTGAT 224
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerAla 67
|||||
225 GTAAGTGTGTGGGAGACACAGCTATTAACCCAGCTGAATCCCGGCT 274
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
275 CAGATACCAAGACACACTCCAGAGCCAGACTCTCTGTGCGCTGAGACA 324
84 erValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
|||||
325 GCGTTACAACTGATGACAGCGCCACCTACTCTGTGCGAAGCTTACG 374
101 GlysPseVal.....ProTyrGlyLeuAspTyr..... 110
|||||
375 GCTGTAGCCGCTACTATGATGTTGCTTATGATGATGATGATGATGATG 424
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```

111 .TriPserProglyLeuLeuLeuThrValSerSer 121
||||: ||||||:|||||
425 CTGGGGCCAAAGACTCCTGGTCACCGCTCTCTCA 458

seq_name: gb_est2:BF606302

seq_documentation_block:
LOCUS      BF606302                495 bp    mRNA    linear    EST 25-APR-2001
DEFINITION 273305 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BF606302
VERSION     BF606302.1  GI:11706773
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 495)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
            G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Perteau,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
21180013
COMMENT    Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 60 row: G column: 12
Seq primer: ATTAGGTGACACTATAG.

FEATURES
            source
            1..495
                /organism="Bos taurus"
                /db_xref="taxon:9913"
                /clone_lib="MARC 3BOV"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                library made from pooled tissue from marrow, alveolar
                macrophage, ovary, fetal semitendinosus muscle, and fetal
                longissimus muscle."
BASE COUNT  104 a      152 c      128 g      111 t
ORIGIN
alignment_scores:
            Quality: 438.00      Length: 127
            Ratio: 4.093      Gaps: 2
Percent Similarity: 84.252      Percent Identity: 71.654

alignment_block:
US-09-786-015-2 x BF606302 ..
Align seq 1/1 to: BF606302 from: 1 to: 495

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||
79 CAGGTGACCTGCGGAGTGGGGCCAGCCTGGTGAAGCCCTCACAGAC 128
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrgly 34
|||||:|||||:|||||:|||||:|||||:|||||

```

```

129 CCTCTCCCTCAGCTGCAGACGACCTCGATTCTCATGAGCGCCTAATACTA 178
34 alserTPvalArgGlnAlaProGlyLysAlaLeuGlnGluTPLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||
179 TAGCCTGGGTCGCCAGGCTCCGGGGAAGGCGCTGGAGTGGCTTGGTGT 228
51 ValSerSerGlyAlaLeuThrAlaTyraAsnThrAlaLeuGlnSerArgLe 67
|||||:|||||:|||||:|||||:|||||:|||||
229 ATAGTAGTGGGGAAGACATGCTTAACCCAGCCCTGGAATCCGGCT 278
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||:|||||:|||||:|||||:|||||:|||||
279 CAGGTCACCAAGACACTCCAGAGCCAGATTCTCTGTCACTTAGCA 328
84 erValThrThrGluAspThrAlaLeuTyrcysAlaLysSer...Val 99
|||||:|||||:|||||:|||||:|||||:|||||
329 GCATGACACACTGAGACACGCGCCACATACACTGTGGCAAGGCTTGTT 378
100 AsnGlyAspSerVal.....ProTyrglyLeuAspTyrrTr 111
|||||:|||||:|||||:|||||:|||||:|||||
379 AATGGATCCTAATAGCTGTGTTTATGATGTATATCACTGCATGCTG 428
111 pSerProGlyLeuLeuLeuThrValSerSer 121
|||||:|||||:|||||:|||||:|||||:|||||
429 GGGCCAAAGACTCCTGGTCACCGCTCTCTCA 459

seq_name: gb_est2:BE485907

seq_documentation_block:
LOCUS      BE485907                502 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 173199 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE485907
VERSION     BE485907.1  GI:9605440
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 502)
AUTHORS   Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,R.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@lpsl.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 131 row: G column: 6
Seq primer: ATTAGGTGACACTATAG.

FEATURES
            source
            1..502
                /organism="Bos taurus"
                /db_xref="taxon:9913"
                /clone_lib="BARC 5BOV"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                library made from pooled mRNA isolated from mammary
                tissues at eight physiological, developmental, and disease
                states."
BASE COUNT  109 a      154 c      129 g      110 t
ORIGIN

```

## alignment\_scores:

Quality: 434.00 Length: 130  
Ratio: 3.945 Gaps: 2  
Percent Similarity: 84.615 Percent Identity: 68.462

## alignment\_block:

US-09-786-015-2 x BE485907 ..

Align seg 1/1 to: BE485907 from: 1 to: 502

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValIysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 CAGGTGACAGTGGCGGAGTCGGGCCAGCGCTGGTAAGCCCTCACAGAC 127
17 rLeuSerLeuThCysThValSerGlyPheSerLeuThLysTyGlyGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 CCTCTCCCTCACCTGCACGGTCTCTGATTCTCATTAAGCAGCTATGCTG 177
34 aISerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 TAAGCTGGGTCCGCCAGGCTCCAGGGAAGGCGCTGGAGTGCCTGGTGCT 227
51 ValSerSerGlyAlaLeuThAlaTyAsnThAlaLeuGlnSerArgLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
228 ATAACTAGTGTGGTAGTACAGACTATTAAGCTGAGCCCTGAATTCGGGCT 277
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
278 CAGCACCACCAAGACACTCCAAAGCCAAAGTCTCTGTCTGAGTACGCA 327
84 erValThrThrGlnAspThrAlaIleTyTyrcysAlaLysSerValasn 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 GCCTGACACTGAGGACAGCGCCACATCTCTGTCTGCAAAAAACAATCT 377
101 .....GlyAspSerValProTyGlyGlye 108
|||||:|||||:|||||:|||||:|||||:|||||:
378 AATGTTAATACCTTGAAATTGTGGTGGTGGAGCGATGACACTAC...GT 424
108 uAspTyrrTrpSerProGlyLeuLeuLeuThValSerSer 121
|||||:|||||:|||||:|||||:|||||:|||||:
425 CGATGCTCTGGGGCCAAGACTCTGTGTGACCCGTCTCTCA 464
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seq\_name: gb\_est2:BE845758

seq\_documentation\_block:

LOCUS BE845758 549 bp mRNA linear EST 25-SEP-2000

DEFINITION 232868 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE845758

VERSION BE845758.1 GI:10282582

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 549)

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tadsejps1.barc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -m1nsc0re 18  
and -m1nmatch 12 options.

PCR primers

FORWARD: AGCAACAGCTATGACCAT

## BACKWARD: GTTTTCCAGTCAGCAGC

Plate: 113 row: J column: 9  
Seq primer: ATTTAGTGACCTATGAT.

## FEATURES

source

Location/Qualifiers

1..549

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_lib="BARC 5BOV"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states"

BASE COUNT 114 a 167 c 151 g 117 t

ORIGIN

## alignment\_scores:

Quality: 434.00 Length: 128  
Ratio: 4.019 Gaps: 3  
Percent Similarity: 84.375 Percent Identity: 71.094

## alignment\_block:

US-09-786-015-2 x BE845758 ..

Align seg 1/1 to: BE845758 from: 1 to: 549

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1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValIysProSerGlnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 CAGGTGACAGTGGCGGAGTCGGGCCAGCGCTGGTAAGCCCTCACAGAC 127
17 rLeuSerLeuThCysThValSerGlyPheSerLeuThLysTyGlyGly 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 CCTCTCCCTCACCTGCACGGTCTCTGATTCTCATTAAGCAGCTATGCTG 177
34 aISerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 TAAGCTGGGTCCGCCAGGCTCCAGGGAAGGCGCTGGAGTGCCTGGTGCT 227
51 ValSerSerGlyAlaLeuThAlaTyAsnThAlaLeuGlnSerArgLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
228 ATAACTAGTGTGGTAGTACAGACTATTAAGCTGAGCCCTGAATTCGGGCT 277
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
278 CAGCACCACCAAGACACTCCAAAGCCAAAGTCTCTGTCTGAGTACGCA 327
84 erValThrThrGlnAspThrAlaIleTyTyrcysAlaLysSer..... 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 GCCTGACACTGAGGACAGCGCCACATCTCTGTCTGCAAAAAATTGCTGAT 377
99 .....ValasnGlyAspSerValProTy.....GlyLeuAspTy 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 AGGTGCTGTGTGTGTGAT...TATAGTTATCTGTGTGTCGGACAAAGTGC 424
110 rTrpSerProGlyLeuLeuLeuThValSerSer 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
425 CTGGGGCCAAGACTCTGTGTCACCGTCTCTCA 458
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seq\_name: gb\_est2:BE476735

seq\_documentation\_block:

LOCUS BE476735 489 bp mRNA linear EST 28-AUG-2000

DEFINITION 160120 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE476735

VERSION BE476735.1 GI:9596268

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 489)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCCAGCAGCAGC  
Plate: 28 row: J column: 21  
Seq primer: ATTTAGTGACACTATAG.  
FEATURES  
source 1..489  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."  
BASE COUNT 107 a 150 c 128 g 104 t  
ORIGIN  
alignment\_scores:  
Quality: 433.50 Length: 121  
Ratio: 4.051 Gaps: 1  
Percent Similarity: 88.430 Percent Identity: 72.727  
alignment\_block:  
US-09-786-015-2 x BE476735 ..  
Align seg 1/1 to: BE476735 from: 1 to: 489  
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGln 17  
|||||  
82 CAGGTGCAGCTGCGGAGTGGGCGCCAGCCTGTGAAGCCCTCAGAC 131  
17 rLeuSerLeuThrcySerThrValSerGlyPheSerLeuThrLysTyrGly 34  
|||||  
132 CCGTCTCCCTACCTGCACGGGTCTCGATTCTCATTAAGCATATATAGTG 181  
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnuTrpLeuGlyGly 50  
|||||  
182 TAAACTGGTGGCCGAGCTCCAGGAAGGCGCTGGAGTGGCTGGGTGC 231  
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67  
|||||  
232 ATTAAGAGTGGTGAAGCACAGGCTATTAACCCAGCCCTGAATCCCGGCT 281  
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84  
|||||  
282 CAGCATCCACCAAGAGCAACATCAAGACCAGGCTCTCTCGGTGAGCA 331  
84 erValThrThrGlnuAspThrAlaAlaLeuTyrGlySerAlaLysSerValAsn 100  
332 GCGGTGACCTGAGGACACACATATCTGTGCAAGAGCGTTGGT 381  
101 GAlAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117  
|||||  
382 GGATATAGTACT...TATACATATATATACCTGGGCGCAAGACTCTCTG 428

117 urhValSerSer 121  
:|||||  
429 CACCGTCTCCTCA 441  
seq\_name: gb\_est2:BE588903  
seq\_documentation\_block:  
LOCUS BE588903 595 bp mRNA linear EST 28-AUG-2000  
DEFINITION 194569 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE588903  
VERSION BE588903.1 GI:9841942  
KEYWORDS EST.  
SOURCE cow.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 595)  
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and Wells,K.D.  
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCCAGCAGCAGC  
Plate: 121 row: C column: 10  
Seq primer: ATTTAGTGACACTATAG.  
FEATURES  
source 1..595  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."  
BASE COUNT 119 a 178 c 167 g 131 t  
ORIGIN  
alignment\_scores:  
Quality: 433.00 Length: 133  
Ratio: 3.936 Gaps: 3  
Percent Similarity: 82.707 Percent Identity: 67.669  
alignment\_block:  
US-09-786-015-2 x BE588903 ..  
Align seg 1/1 to: BE588903 from: 1 to: 595  
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGln 17  
|||||  
64 CAGGTGCAGCTGCGGAGTCAAGGCTGGTGAAGCCCTCAGAC 113  
17 rLeuSerLeuThrcySerThrValSerGlyPheSerLeuThrLysTyrGly 34  
|||||  
114 CCGTCTCCCTACCTGCACGGGTCTCGATTCTCATTAAGCATATATAGTG 163  
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnuTrpLeuGlyGly 50  
|||||  
164 TAAACTGGTGGCCGAGCTCCGGAAGGACATGAGTGGGTTGGGCT 213



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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
BASE COUNT      109 a      150 c      149 g      110 t
ORIGIN

alignment_scores:
  Quality:      430.50      Length:      134
  Ratio:        3.950      Gaps:      3
  Percent Similarity: 81.343      Percent Identity: 68.657

alignment_block:
US-09-786-015-2 x BE476121 ..

Align seg 1/1 to: BE476121 from: 1 to: 518

1  GlnValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh 17
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
97 CAGGTGCAGCTGCCGAGTCGGGCCAGCCTGGTGAAGCCCTCACAGAC 146

17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrgly 34
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
147 CCTCTCCCTCACCTGACAGCGTCTGATCTCATTTGAGCAGCTATGCTG 196

34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
197 TAAGCTGGATCGCCAGGCTCCAGGGAAGGCGTGGAGTGGCTGGTGGT 246

51 ValSerSerGlyAlaLeuThralaTyraThrAlaLeuGlnSerArgLe 67
   :: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
247 ATACACAGTGGTGAAGACACAGGCTATTAACCCACCCCTGAATCCGGCT 296

67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
297 CAGCATCCACCAAGACAACCTCCAAAGAGCCAGTCTCGCTGACATGAGACA 346

84 erValThThrGluAspThrAlaIleTyrycysAlaLysSerVal... 99
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
347 GCGTGACACTGAGGACACGGCCACATACCTGTGCAAAAAGTTCTTAT 396

100 .....AsnGlyAspSer.....ValProTyrgly..... 107
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
397 GGTGGTGGTGGCGATAGTGGTACTGTGTGGGCTTATGTCATGCTTA 446

108 .....LeuAspTyrrTpSerProGlyLeuLeuLeuThrValSerS 121
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
447 TAGGACACTAGCTGATGCTGGGCGCAAGAGACTCTGTGTCAACCGTCTCT 496

121 er 121
   ||
497 CA 498

seq_name: gb_est2:BG692944

seq_documentation_block:
LOCUS      BG692944      513 bp      mRNA      linear      EST 02-MAY-2001
DEFINITION  342818 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG692944
VERSION    BG692944.1 GI:13934764
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE  1 (bases 1 to 513)

```

```

AUTHORS      Sonstegard, T.S., Capuco, A.V., Van Tassel, C.P., Ashwell, M.S. and
              Wells, K.D.
TITLE        Mapping of Expressed Sequence Tags from a normalized bovine mammary
              gland cDNA library
JOURNAL      Unpublished (2000)
COMMENT      Contact: Sonstegard TS
              USD, ARS, Beltsville Agricultural Research Center
              Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
              Tel: 301 504 8416
              Fax: 301 504 8414
              Email: tads@psi.barc.usda.gov
              Single pass sequencing. Bases called and alt trimmed with phred
              v0.980904.e. Vector identified by cross-match with the -minscore 18
              and -mismatch 12 options.
PCR Primers  FORWARD: AGGAACAGCTATGACAC
              BACKWARD: GTTTCCTCAGCAGAC
              Plate: 43 row: J column: 13
              Seq primer: ATTAGTGCACATATAG.
FEATURES
  source
    1..513
    /organism="Bos taurus"
    /db_xref="taxon:9913"
    /clone_lib="BARC 5BOV"
    /tissue_type="pooled"
    /lab_host="DH10B"
    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
    Library made from pooled mRNA isolated from mammary
    tissues at eight physiological, developmental, and disease
    states."
BASE COUNT      106 a      155 c      139 g      113 t
ORIGIN

alignment_scores:
  Quality:      428.00      Length:      133
  Ratio:        3.891      Gaps:      3
  Percent Similarity: 82.707      Percent Identity: 69.925

alignment_block:
US-09-786-015-2 x BG692944 ..

Align seg 1/1 to: BG692944 from: 1 to: 513

1  GlnValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh 17
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
64 CAGGTGCAGCTGCCGAGTCGGGCCAGCCTGGTGAAGCCCTCACAGAC 113

17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrgly 34
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
114 CCTCTCCCTCACCTGACAGCGTCTGATCTCATTTGAGCAGCTATGCTG 163

34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
164 TAAGCTGGTCCGCCAGGCTCCAGGGAAGGCGCTGGAGTGGCTCGAGGT 213

51 ValSerSerGlyAlaLeuThralaTyraThrAlaLeuGlnSerArgLe 67
   :: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
214 ATTCGACAGTAGTGAACACACAGCCTATTAACCCACCCCTGAATCCGGCT 263

67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
264 CAGCATCCACCAAGACAACCTCCAAAGAGCCAGTCTGTGTCAGTGAGCA 313

84 erValThThrGluAspThrAlaIleTyrycysAlaLysSer..... 98
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
314 GCGTGACACTGAGGACACGGCCACATACCTGTGCAAAAAGTAGTTAT 363

99 .....ValAsnGlyAspSerValPro.....Tyrgly.. 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
364 AGTGGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTAA 413

108 .....LeuAspTyrrTpSerProGlyLeuLeuLeuThrValSerS 121

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414 TAATTACTGATGCTGGGGCCAGGACTCTGTCACCGCTCCCA 462

seq\_name: gb\_est2:BF230469

seq\_documentation\_block:

LOCUS BF230469 501 bp mRNA linear EST 14-NOV-2000  
DEFINITION 252126 BARC SBOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF230469  
VERSION BF230469.1 GI:11168474  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 501)  
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and  
Wells,K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCAGCAGC  
Plate: 110 row: J column: 3  
Seq primer: ATTTAGTGACACTATG.

FEATURES  
source  
1..501  
Location/Qualifiers

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC SBOV"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPOR6; Site\_1: XbaI; Site\_2: XhoI;  
library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 104 a 153 c 132 g 112 t  
ORIGIN

alignment\_scores:

Quality: 427.50 Length: 126  
Ratio: 4.033 Gaps: 2  
Percent Similarity: 84.127 Percent Identity: 69.841

alignment\_block:

US-09-786-015-2 x BF230469

Align seg 1/1 to: BF230469 from: 1 to: 501

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValIysProSerGlnTh 17  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
80 CAGGTGAGCTGGGGAGTGGGGCCAGGCTGTGTAAGCCCTCACAGAC 129  
17 rLeuSerLeuThCysThrValSerGlyPheSerLeuThIlySTyGlyV 34  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
130 CCTCTCCCTCAGCTGCACGCTCTCTGATTCATTCAGCAGCTATACTG 179  
34 aIseTPrValArgGlnAlaProGlyIysAlaLeuGlnUTrPleuGlyGly 50  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
180 TAAGCTGGTCCGCAAGCTCCAGGGAAGGCGCTGGAATGGTTGTTCAT 229

51 ValSerSerGlyAlaLeuThrAlaTyAsnThrAlaLeuGlnSerArgle 67  
::: |||::: || ||||| |||||:|||||:|||||  
230 ATAGAGATGATGAGACACATACTATACCCAGCCCTGAATCCCTCT 279  
67 uSerValThArgAspThSerIySerGlnPheSerLeuSerLeuSers 84  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
280 TAGCATCCACAGGACAACTCAAGAGCCAAAGTCTCTCTGTCAGTAGACA 329  
84 eValThrThrGluAspThrAlaIleTyTyrcyAlaIyServal... 99  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
330 GCGTGACACCTGAGACACAGCCACATCACTGTGAGTAGTTGTGT 379  
100 AsnGlyAspSerValProTyGlyLeuAspTyf.....TpsE 112  
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
380 GGTGAGATGCTCTTTATTATGTTGTTACTTATGTCCCATGCTGGGG 429  
112 rProGlyLeuLeuLeuThrValSerSer 121  
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
430 CCAAGACTCTCTGTCACCGCTCCCTCA 457

seq\_name: gb\_est2:BE480721

seq\_documentation\_block:

LOCUS BE480721 509 bp mRNA linear EST 28-AUG-2000  
DEFINITION 165931 BARC SBOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE480721  
VERSION BE480721.1 GI:9600254  
KEYWORDS EST.  
SOURCE  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 509)  
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and  
Wells,K.D.  
Mapping of Expressed Sequence Tags from a normalized bovine mammary  
gland cDNA library  
Unpublished (2000)  
Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCAGCAGC  
Plate: 17 row: L column: 19  
Seq primer: ATTTAGTGACACTATG.

FEATURES  
source  
1..509  
Location/Qualifiers

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC SBOV"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPOR6; Site\_1: XbaI; Site\_2: XhoI;  
library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 110 a 154 c 130 g 115 t  
ORIGIN

alignment\_scores:

Quality: 427.50 Length: 123  
Ratio: 4.071 Gaps: 2  
Percent Similarity: 85.366 Percent Identity: 72.358

## alignment\_block:

US-09-786-015-2 x BE480721 ..

Align seg 1/1 to: BE480721 from: 1 to: 509

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1 GluValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
  |||.....|
91 CAGGTGACGCTGCGGAGTCGGCCCAAGCCTGGTGAAGCCCTCAGAC 140
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrgly 34
  |||.....|
141 CCTCTCCCTCACCCTGACGGGTCTGTGATCTCTATTAAAGCAGCATATG 190
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
  |||.....|
191 TAGGCTGGGTCCGCGCAGCTCCAGAAAGGCGTGAATGCTGCTGCTC 240
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgly 67
  |||.....|
241 ATACATAGTGTGGAAACACAGACTATTAACCGCCCTGAATGCGGCT 290
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
  |||.....|
291 CATCATCACCAGGACAACTCCAGAGCAAGTCTCTATCACTGAGCA 340
84 eValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
  |||.....|
341 GCGGACACAGTGAAGACACGCGCACATCACTGTGCAGATGATTATTAT 390
101 GlyAsp.....SerValProTyrGlyLeuAspTyrTrpSerProGlyLe 115
  |||.....|
391 GGTATGTTGTTATTTCTTGAATTTCTCTGTGGAC...TGGGGCCAGGACT 437
115 uLeuLeuThrValSerSer 121
  |||.....|
438 CCTGGCCACGCTCTCCCA 456
seq_name: gb_est2:BE588530

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## seq\_documentation\_block:

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LOCUS      BE588530                581 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 193837 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE588530
VERSION    BE588530.1 GI:9841569
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.

```

REFERENCE 1 (bases 1 to 581)

AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and Wells,K.D.

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross-match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCAGCAG

Plate: 116 row: D column: 22

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1..581

/organism="Bos taurus"

```

/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPOR6; Site.1: XbaI; Site.2: XhoI;
library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

```

alignment\_scores: Quality: 427.50 Length: 132

Percent Similarity: 81.818 Ratio: 3.958 Gaps: 2

Percent Identity: 68.182

US-09-786-015-2 x BE588530 ..

Align seg 1/1 to: BE588530 from: 1 to: 581

```

1 GluValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
  |||.....|
61 CAGGTGACGCTGCGGAGTCGGCCCAAGCCTGGTGAAGCCCTCAGAC 110
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTrgly 34
  |||.....|
111 CCTCTCCCTCACCCTGACGGGTCTGTGATCTCTATTAAAGCAGCATATG 160
34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
  |||.....|
161 TAACTGGGTCCGCGCAGCTCCAGAAAGGCGTGAATGCTGCTGCTGCTG 210
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgly 67
  |||.....|
211 ATACATAGTGTGGAAACACAGACTATTAACCGCCCTGAATGCGGCT 260
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
  |||.....|
261 CAGCATCACCAGGACAACTCCAGAGCAAGTCTCTATCACTGAGCA 310
84 eValThrThrGluAspThrAlaIleTyrTrpCysAlaLysSerValAsn 100
  |||.....|
311 GCGGACACAGTGAAGACACGCGCACATCACTGTGCAGAAAGCTGTGCT 360
101 GlyAspSerVal.....ProTyrGlyLeuAs 109
  |||.....|
361 GGTGCTGTTAGTGTGTTATGTTTATCTTAAATGCTTATGTTTCGA 410
109 pTyr.....TrpSerProGlyLeuLeuLeuThrValSerSer 121
  |||.....|
411 TTACGTGATGCTCGGGGCCAAGACATCTGCTGACCGCTCTCCCA 456

```



---

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 12, 2002, 09:25:38 ; Search time 52.21 seconds

(without alignments)  
236.146 Million cell updates/sec

Title: US-09-786-015-4

Perfect score: 564

Sequence: 1 QDVLTGPSVSSVSGSLGRVSI.....SYOSTYSGVFSGSGRLTVLG 111

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A.Geneseq\_032802:\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
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5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
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11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*  
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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564	100.0	111	21	AAV82529
2	389	69.0	147	22	AAV82507
3	388.5	68.9	236	22	AAV82509
4	387	68.6	249	22	ABG12886
5	386	68.4	110	22	AAU02620
6	385.5	68.4	109	21	AAV92505
7	385	68.3	113	22	AAV65569
8	385	68.3	117	22	AAV80216
9	383.5	68.0	112	21	AAV82208
10	382	67.7	111	22	AAV62963
11	382	67.7	249	21	AAV36083

12	381.5	67.6	246	21	AAV58235
13	381	67.6	110	22	AAV02577
14	381	67.6	111	22	AAV62857
15	381	67.6	111	22	AAV65319
16	381	67.6	113	22	AAV34276
17	381	67.6	235	14	AAV65320
18	380.5	67.5	130	22	AAV65328
19	380	67.4	111	18	AAV13528
20	380	67.4	111	20	AAV43257
21	380	67.4	131	21	AAV31535
22	379.5	67.3	110	21	AAV95182
23	379.5	67.3	112	18	AAV08488
24	379.5	67.3	118	22	AAV65555
25	379.5	67.3	242	21	AAV95209
26	379	67.2	235	22	AAV36212
27	379	67.2	251	22	ABG12291
28	378.5	67.1	112	21	AAV39520
29	377	66.8	110	22	AAV80222
30	377	66.8	111	15	AAV45606
31	377	66.8	111	18	AAV08492
32	377	66.8	249	20	AAV06713
33	377	66.8	258	18	AAV08487
34	377	66.8	262	20	AAV97890
35	376.5	66.8	310	20	AAV83324
36	376	66.7	110	20	AAV78423
37	376	66.7	110	20	AAV78424
38	376	66.7	110	20	AAV78425
39	376	66.7	110	20	AAV78426
40	376	66.7	110	20	AAV78430
41	376	66.7	111	20	AAV78431
42	376	66.7	111	20	AAV43256
43	375	66.5	110	21	AAV96061
44	375	66.5	132	22	AAV65561
45	375	66.5	242	20	AAV21881

## ALIGNMENTS

RESULT 1	AAV82529	standard; Protein; 111 AA.
ID	AAV82529	
AC	AAV82529	
XX		
DT	13-JUL-2000	(first entry)
XX		
DE	Carcinoembryonic antigen affinity antibody light chain variable region.	
XX		
KW	Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;	
KW	tumour associated antigen; anti-carcinogenic; cytostatic;	
KW	cancer therapy.	
XX		
OS	Ovis sp.	
XX		
PN	WO200012556-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	20-AUG-1999;	99WO-GB02729.
XX		
PR	28-AUG-1998;	98GB-0018915.
XX		
PA	(KSBI-) KS BIOMEDIX LTD.	
XX		
PI	Harrison PJ;	
XX		
DR	WPI: 2000-375618/32.	
XX		
DR	N-PSDB; AAA08401.	
XX		
PT	A new high-affinity monoclonal antibody that is characterized by an	
XX	acid-washed enzyme-linked immunosorbent assay for use in cancer therapy	

PS Claim 8; Page 16; 21pp; English.

XX The present invention describes a high-affinity monoclonal antibody  
CC characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).  
CC The antibody is used in cancer therapy. Association of the new antibody  
CC with an antigen is favoured over dissociation in vivo and they therefore  
CC have longer localisation times at target sites, resulting in a higher  
CC concentration of antibodies localised at the target sites. Targeting the  
CC antibody to a site in vivo is improved. The concentration of antibody  
CC does not need to be too high which reduces side-effects and costs of  
CC therapy. The present sequence represents the light chain variable region  
CC of a monoclonal antibody having affinity for carcinoembryonic antigen  
CC (CEA, a tumour associated antigen), which is used in the exemplification  
CC of the present invention.

SQ Sequence 111 AA;

QY Query Match 100.0%; Score 564; DB 21; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2.3e-38;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 QDVLTPSSVSGSLGQRVITCGSSSSNIGNAYVGYOQVPGAPRLILSATTDRAAGI 60  
1 qdvltpssvsgslgqrvtscgsssnlgmavgyvqvpaprlilisattdraagi 60

OY 61 PDRFGSRSGNTATLTISSLOAEDEADYYCASYQSTYSGVFSGRTLTVLG 111  
|||||  
61 pdrfgsrsgntatltilssloaedeaddyccasyqstysgfvsgfsgrtlvtlg 111

DB 61 pdrfgsrsgntatltilssloaedeaddyccasyqstysgfvsgfsgrtlvtlg 111

RESULT 2  
AAM39507 standard; Protein; 147 AA.

XX AAM39507;  
XX  
XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2652.

XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.  
XX 25-APR-2000; 2000US-0552317.  
XX 09-JUL-2000; 2000US-0598042.  
XX 19-JUL-2000; 2000US-0620312.  
XX 03-AUG-2000; 2000US-0653450.  
XX 14-SEP-2000; 2000US-0662191.  
XX 19-OCT-2000; 2000US-0693036.  
XX 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang Z, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.  
XX N-PSDB; AAI58663.

XX Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
PS  
XX Example 4; SEQ ID NO 2652; 10078bp; English.

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.

SQ Sequence 147 AA;

QY Query Match 69.0%; Score 389; DB 22; Length 147;  
Best Local Similarity 67.3%; Pred. No. 3.5e-24;  
Matches 76; Conservative 16; Mismatches 19; Indels 2; Gaps 1;

DB 1 QDVLTPSSVSGSLGQRVITCGSSSSNIGNAYVGYOQVPGAPRLILSATTDRAAGI 60  
1 qdvltpssvsgslgqrvtscgsssnlgmavgyvqvpaprlilisattdraagi 60

OY 20 qvyltqpsvsgslgqrvtscgsssnlgmavgyvqvpaprlilisattdraagi 79

OY 61 PDRFGSRSGNTATLTISSLOAEDEADYYCASYQSTYSGVFSGRTLTVLG 111  
|||||  
61 pdrfgsrsgntatltilssloaedeaddyccasyqstysgfvsgfsgrtlvtlg 111

DB 80 pdrfgsrsgntatltilssloaedeaddyccasyqstysgfvsgfsgrtlvtlg 132

RESULT 3  
AAB36209 standard; protein; 236 AA.

XX AAB36209;  
XX  
XX 15-FEB-2001 (first entry)

DE Human immune system associated protein HISAP-7.

XX Human; immune system associated protein; HISAP-7; immune disorder;  
KW infection; autoimmune disease; cancer.

XX Homo sapiens.

XX US6135941-A.

XX 24-OCT-2000.

XX 27-MAR-1998; 98US-0049672.  
XX 27-MAR-1998; 98US-0049672.

PA (INCY-) INCYTE PHARM INC.

PI Tang YF, Yue H, Lai P, Corley NC, Guegler KJ, Baughn MR;  
PI Hillman JL, Au-Young J;

XX WPI: 2001-030926/04.  
XX N-PSDB; AAC6525.

PT New human immune system associated proteins (HISAP) and polynucleotides  
PT encoding the HISAP, useful for diagnosing, treating or preventing  
PT immune or cell proliferative disorders or infections -

to restore normal activity of (II) or to treat disease states involving

CC obesity related diseases. The antibodies can be used to deliver drugs or



Query Match	68.3%	Score 385;	DB 22;	Length 113;
Best Local Similarity	67.3%	Pred No. 5.7e-24;		
Matches 76; Conservative	15;	Mismatches 20;	Indels 2;	Gaps 1

RESULT	8
AAG80216	
ID	AAG80216 standard; Protein; 117 AA

KM Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;  
KM glutamate decarboxylase; diabetes mellitus type 1; stiff-man syndrome;  
KM polyglutamine syndrome; autoimmune disorder; IA2; GAD65;  
KM variable region; heavy chain; MICA-6.

PD 31-OCT-2001

PF 29-MAR-2001; 2001EP-0107702.

PR 10-APR-2000; 2000DE-1017782.  
PR 25-MAY-2000; 2000DE-1025840.

PA (LABO-) LABOR KOCH MERK GMBH.

PI Richter W, Rickert M, Rapp I, Dangel W;

DR WPI; 2001-640702/74.

XX

PT glutamate decarboxylase and islet cell antigen -

CC This invention describes a novel fusion protein (I) that has, at its  
CC N-terminus, one or more epitopes that bind specifically to autoantibodies  
CC (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or  
CC more epitopes that bind specifically to autoantibodies (Ab) directed against  
CC the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding  
CC it, vectors containing (II) and transformed cells, are useful for  
CC diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome,  
CC polyglandular autoimmune syndrome or other autoimmune conditions  
CC associated with AAb against GAD65 or IA2. (I) provides a rapid and simple  
CC diagnosis of high specificity and sensitivity, capable of recognizing  
CC antibodies against both IA2 and GAD65, simultaneously. Unlike known  
CC fusions, where the GAD65 component is at the N-terminus, (I) contains  
CC correctly folded conformational epitopes that can react with most MICA  
CC autoantibodies. This sequence represents the human autoantibody MICA-6  
CC variable region heavy chain used in the method of the invention.  
CX  
XX Sequence 117 AA:

Query Match	68.3%	Score 385	DB 22	Length 117
Best Local Similarity	66.1%	Pred. No. 5.9e-24		
Matches 72	Conservative 16	Mismatches 21	Indels 0	Gaps 0

[illegible]

RESULT	9
AAB52208	
ID	AAB52208 standard; Protein; 112 AA

AC AAB52208;

DT 22-FEB-2001 (first entry)

DE Human anti-HBs antibody light chain protein fragment SEQ ID 30.

KW Anti-hepatitis B monoclonal antibody; human; hepatitis B; prevention;

XX

XX

XX

XX

XX

XX

PA (MEIP ) MEIJI MILK PROD CO LTD

DR WPI; 2000-675345/66

XX

PT hepatitis B -

PS Claim 21; page 18; 27pp; Japanese

CC This invention relates to a human anti-hepatitis B monoclonal antibody

CC AAB52210 are fragments of the anti-hepatitis B light and heavy chains.

CC Also included in the invention are PCR primers AAC96956 - AAC96977 which  
CC are used in the construction of the antibody. The antibody exhibits  
CC antiinflammatory, and hepatotrophic activity, and can be used in a drug  
CC effective at preventing hepatitis B infection.

XX Sequence 112 AA:

Query Match 68.0%; Score 383.5; DB 21; Length 112;  
Best Local Similarity 67.9%; Pred. No. 7.4e-24;  
Matches 76; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 QDVLTPSSVSGSLGQRVSTTCGSSSNIGGNAYGVGYQVPGSAPRLISATTDASGI 60  
D 1 qsvltqpsvsgspgqrlstscigsssnigaygdyvgwqqlpgtapklllfvnlrpsgv 60

QY 61 PDRFSGSRGNTATLTFTSSLOAEDEADYGCASYQSTYSG-VFGSGTRLVIG 111  
D 61 pdrfsgskgtsalstltglaedeadygcgsydsstlsgygtlcvlvg 112

RESULT 10

AAG62963  
ID AAG62963 standard; Protein; 111 AA.

XX AAG62963;

01-OCT-2001 (first entry)

DE Amino acid sequence of variable light chain fragment of clone G102.

XX Antibody; light chain; VL; amyloid protein; blood brain barrier;  
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;  
KM transferrin receptor; neurological disease; Alzheimer's disease;  
XX prion disease; AIDS-related dementia; epilepsy; brain injury.

OS Homo sapiens.

XX WO200144300-A2.

PN 21-JUN-2001.

PD 27-NOV-2000; 2000MO-GB04501.

XX 13-DEC-1999; 99US-0170599.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PA Webster C, Osbourn J, Ward G, Miller K;

PI WPI, 2001-398131/42.

XX N-PDB; AAH42407.

PT Mixture or panel of antibodies for selecting specific binding members  
PT that cross the blood brain barrier, for use in delivering different  
PT molecules and treating neurological diseases

XX Claim 1; Page 106; 109pp; English.

XX The present sequence represents an antibody variable light chain (VL)  
CC fragment. The fragment is used to produce a mixture or panel of 5  
CC different specific binding members, each comprising an antibody VH  
CC and/or VL variable domain and capable, when displaying on the surface  
CC of filamentous bacteriophage particles or in the case of a specific  
CC binding member comprising the D5 VH and/or VL variable domain when  
CC bound to human serum amyloid protein, to pass through a mammalian  
CC blood brain barrier (BBB). The panel is useful for the selection of  
CC specific binding members with a desired property such as ability to  
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,  
CC ability to bind areas of inflammation in the brain or BBB breakdown or  
CC ability to bind intracellular adhesion molecules and to bind transferrin  
CC receptor. The antibodies are useful in diagnosis, prophylaxis and  
CC treatment of human or animal body, including neurological diseases, such

CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy  
CC and traumatic brain injury and any diseases involving inflammation  
CC occurring within the brain or central nervous system.

XX Sequence 111 AA:

Query Match 67.7%; Score 382; DB 22; Length 111;  
Best Local Similarity 64.9%; Pred. No. 9.7e-24;  
Matches 72; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 QDVLTPSSVSGSLGQRVSTTCGSSSNIGGNAYGVGYQVPGSAPRLISATTDASGI 60  
D 1 qsvltqpsvsgspgqrlstscigsssnigaygdyvgwqqlpgtapklllfvnlrpsgv 60

QY 61 PDRFSGSRGNTATLTFTSSLOAEDEADYGCASYQSTYSGVFGSGTRLVIG 111  
D 61 pdrfsgskgtsalstltglaedeadygcgsydsstlsgygtlcvlvg 111

RESULT 11

AAB36083  
ID AAB36083 standard; Protein; 249 AA.

XX AAB36083;

16-FEB-2001 (first entry)

DE Recombinant human antibody scFv TN11.

XX Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;

XX CTN-C.

OS Homo sapiens.

XX WO200063699-A1.

PN 26-OCT-2000.

PD 19-APR-2000; 2000MO-EP03550.

XX 20-APR-1999; 99IT-FI00094.

XX (PHIL-) PHILGREN SRL.

PA Zardi L;

PI WPI; 2000-687225/67.

XX N-PDB; AAC67868.

PT Ligands used for diagnosis and treatment of human neoplasias, are  
PT capable of identifying the tenascin-C isoform containing domain C of  
PT tenascin-C

XX Disclosure; Page 5-6; 31pp; English.

XX The present sequence is a recombinant human antibody scFv. Antibody  
CC TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope  
CC recognised by TN11 is located inside domain C of TN-C. TN11 is therefore  
CC only capable of recognising TN-C isoforms containing domain C (CTN-C).  
CC TN11 is useful for detecting the presence of TN-C isoforms in vitro or  
CC in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C.  
CC It is useful for the preparation of formulations for the treatment of  
CC human neoplasias.

XX Sequence 249 AA:

Query Match 67.7%; Score 382; DB 21; Length 249;  
Best Local Similarity 64.9%; Pred. No. 2.1e-23;  
Matches 72; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 QDVLTPSSVSGSLGQRVSTTCGSSSNIGGNAYGVGYQVPGSAPRLISATTDASGI 60



Db 139 gqvltgspasvsgpqsdlitcgtcsdgygyvwyqghpqbakpklmlyegsktrpsgv 198  
 QY 61 PRFSGSRSGNTATLTISLQAEDADYVCASQSTYSGVFGSGTRLTVLG 111  
 Db 199 snrtsgsksgnbasltlsglqaeadeaycysyltrstrlvf9g9kklvlg 249

## RESULT 12

AA58235  
 ID AA58235 standard; Protein: 246 AA.

XX  
 AC AA58235;

XX  
 DT 27-MAR-2000 (first entry)

XX  
 DE Internalising anti-c-erbB-2 receptor antibody scFv F5.

XX  
 KW Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;

XX  
 KW HER/neu oncogene; tumour-specific; Internalisation; non-Immunogenic.

XX  
 OS Synthetic.

XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers

FT 31..35  
 FT /note= "Heavy chain variable region (VH) complementarity

FT 50..66  
 FT /note= "VH-CDR2"

FT 99..108  
 FT /note= "VH-CDR3"

FT 157..170  
 FT /note= "Light chain variable region (VL) complementarity

FT 186..192  
 FT /note= "VL-CDR2"

FT 225..235  
 FT /note= "VL-CDR3"

XX  
 PN MO9955367-A1.

XX  
 PD 04-NOV-1999.

XX  
 PE 23-APR-1999; 99WO-US07395.

XX  
 PR 24-APR-1998; 98US-0082953.

XX  
 PR 12-FEB-1999; 99US-0250056.

XX  
 PA (REGC ) UNIV CALIFORNIA.

XX  
 PI Marks JD, Poul MA;

XX  
 DR WPI: 2000-072168/06.

XX  
 DR N-PSDB; AA58235.

XX  
 PT Novel internalizing antibodies used to treat cancer cells -

XX  
 PS Claim 3; Page 81; 85pp; English.

XX  
 CC This sequence represents an internalising humanised antibody,

XX  
 CC scFv F5, which specifically binds to the extracellular domain

XX  
 CC of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.

XX  
 CC The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that

XX  
 CC is bound by F5 antibodies. On binding the c-erbB-2 receptor, the

XX  
 CC antibody is transported into the cell. The c-erbB-2 receptor is a marker

XX  
 CC protein which is overexpressed by 30-50% of breast carcinomas and other

XX  
 CC adenocarcinomas, and thus provides a useful cell surface marker for

XX  
 CC specifically targeting tumour cells. The antibodies of the invention

XX  
 CC are used as tumour-targeting molecules for diagnosis and treatment. The

XX  
 CC antibodies can be attached to effector molecules. The effector molecules

XX  
 CC may include cytotoxins such as ricin, abrin or pseudomonas exotoxin;

XX  
 CC radionuclides; ligands such as growth factors; therapeutic agents such

CC as vinblastine, vindesine or melphalan; ribozymes; or antisense  
 CC molecules. The antibodies may also be used for in vivo or in vitro  
 CC detection and/or quantitation of the c-erbB-2 receptor and thus diagnosis  
 CC and/or localisation of cancers characterised by expression of c-erbB-2.  
 CC Although antibodies have previously been used to target tumour cells,  
 CC their success has been limited. The utility of prior art antibodies has  
 CC been hampered by the paucity of tumour specific antibodies, antibody  
 CC immunogenicity, low binding affinity, and poor tumour penetration.  
 CC Immunogenicity could be avoided and toxicity reduced if high affinity  
 CC tumour specific human antibodies were available. However, the production  
 CC of human monoclonal antibodies using conventional hybridoma technology  
 CC has proven difficult. Also, most of the antibodies produced react with  
 CC antigens that are also common to non-malignant cells, which makes them  
 CC unsuitable for use as tumour-targeting molecules. The antibodies of the  
 CC invention overcome these difficulties, as they are targeted to a  
 CC tumour-specific antigen, and avoid the problem of immunogenicity as they  
 CC are human in origin.

CC  
 SQ Sequence 246 AA:

Query Match 67.6%; Score 381.5; DB 21; Length 246;  
 Best Local Similarity 67.0%; Pred. No. 2.3e-23;  
 Matches 75; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 QDVINQPSVSGSLGQRVSTTCGSSSNIGNAYVGVQVGSAPRLISATDRASGI 60  
 Db 135 gqvltgspasvsgpqsdlitcgtcsdgygyvwyqghpqbakpklmlyegsktrpsgv 194

QY 61 PRFSGSRSGNTATLTISLQAEDADYVCASQSTYSGVFGSGTRLTVLG 111  
 Db 195 snrtsgsksgnbasltlsglqaeadeaycgyfysdls9g9kklvlg 246

## RESULT 13

AAU02577  
 ID AAU02577 standard; Protein: 110 AA.

XX  
 AC AAU02577;

XX  
 DT 29-AUG-2001 (first entry)

XX  
 DE Anti-adipocyte monoclonal antibody light chain, FAT 64.

XX  
 KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;

XX  
 KW heart disease; complementarity determining region; CDR.

XX  
 OS Homo sapiens.

XX  
 PN WO200127279-A1.

XX  
 PD 19-APR-2001.

XX  
 PE 11-OCT-2000; 2000WO-GB03900.

XX  
 PR 12-OCT-1999; 99US-0158812.

XX  
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX  
 PI Edwards BM, Main SH, Vaughan TJ;

XX  
 DR WPI: 2001-282031/29.

XX  
 DR N-PSDB; AAS03477.

XX  
 PT Panel of specific binding members of antibody molecules which bind to

XX  
 PT whole adipocytes is used in the treatment of obesity and obesity

XX  
 PT related diseases -

XX  
 PS Claim 1; Page 141; 182pp; English.

XX  
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid

XX  
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light

XX  
 CC chain, and heavy chain complementarity determining regions (CDR) of the





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 12, 2002, 09:22:50 ; Search time 52.21 Seconds

(without alignments)  
257.421 Million cell updates/sec

Title: US-09-786-015-2

Perfect score: 614

Sequence: 1 OVQLQESGSLVKRSQTLSL.....DSVYGYDYSWSPGLLTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
A.Geneseq\_032802:\*

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- 22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	121	21	AAV82528
2	430	70.0	137	14	AAAR42796
3	417	67.9	142	22	AAAG6523
4	411.5	67.0	120	20	AAV22432
5	411	66.9	129	14	AAAR42798
6	409.5	66.7	137	18	AAW30273
7	406.5	66.2	120	20	AAV22429
8	404.5	65.9	116	17	AAW05823
9	404.5	65.9	120	20	AAV22430
10	404.5	65.9	120	20	AAW05827
11	404.5	65.9	446	17	AAW05829

12	400.5	65.2	120	20	AAV22433
13	393.5	64.1	120	20	AAV22431
14	390.5	63.6	140	18	AAAR22538
15	390	63.5	141	14	AAAR42797
16	389	63.3	119	21	AAV90818
17	388.5	63.3	120	12	AAAR13310
18	388.5	63.3	120	15	AAAR72303
19	388.5	63.3	132	15	AAAR53331
20	388.5	63.3	132	20	AAV28359
21	387	63.0	120	12	AAAR11986
22	385	62.7	119	17	AAAR98492
23	384	62.5	138	13	AAAR29012
24	384	62.5	138	13	AAAR29014
25	384	62.5	256	21	AAV55072
26	384	62.5	260	21	AAV55075
27	384	62.5	367	21	AAV55078
28	384	62.5	381	21	AAV55079
29	384	62.5	519	21	AAV55080
30	384	62.5	546	21	AAV55074
31	384	62.5	626	21	AAV55081
32	384	62.5	640	21	AAV55082
33	383	62.4	119	18	AAAR01584
34	382.5	62.3	138	13	AAAR21406
35	382	62.2	119	19	AAAR21268
36	381	62.1	113	13	AAAR21268
37	381	62.1	123	18	AAW07438
38	380	61.9	249	21	AAV69523
39	379.5	61.8	116	22	AAU07513
40	379.5	61.8	239	18	AAW35561
41	379.5	61.8	239	18	AAW09813
42	379.5	61.8	241	13	AAAR21261
43	379.5	61.8	241	20	AAV08988
44	379.5	61.8	267	11	AAAR04841
45	379.5	61.8	272	13	AAAR21260

#### ALIGNMENTS

RESULT 1	
AAV82528	standard; Protein; 121 AA.
AAV82528:	
13-JUL-2000 (first entry)	
Carcinoembryonic antigen affinity antibody heavy chain variable region.	
Carcinoembryonic antigen; CEA; sheep; monoclonal antibody;	
tumour associated antigen; anti-carcinogenic; cytostatic;	
cancer therapy.	
Ovis sp.	
WO200012556-A1.	
09-MAR-2000.	
20-AUG-1999;	99WO-GB02729.
28-AUG-1998;	98GB-0018915.
(KSBI-) KS BIOMEDIX LTD.	
Harrison PJ;	
WPI: 2000-375618/32.	
N-PDSB; AAA08400.	
A new high-affinity monoclonal antibody that is characterized by an acid-washed enzyme-linked immunosorbent assay for use in cancer therapy	

TM27 antibody VH c  
TM27 antibody VH c  
TM27 antibody VH c  
Partial B13/B14 Ab  
26OF9 hybridoma VL  
HuVh1.3. Syncheli  
Variable heavy cha  
KM-603 heavy chain  
Antibody heavy cha  
Human anti-placent  
NEWM humanised 286  
pUC-RVH-PM1f. Syn  
pUC-RVH-PM1f-4. S  
Interleukin-6 spec  
Single chain Fv pr  
Single chain Fv pr  
Single chain Fv pr  
Single chain Fv pr  
Single chain Fv pr  
Single chain Fv pr  
Single chain Fv pr  
Lead binding Mab 1  
Sequence of the si  
NEWM humanised hea  
Murine VH group 2  
Anti-DNA antibody  
Anti-CD38 antibody  
Antibody gcfv8 hea  
EcoRI-HindIII lase  
VLys-Linker-VHlys  
VH1.3-HuCh1 regio  
pUR4125 VL-Lys-syn  
Two linked VHlys p  
Scrv sequences enc

PS Claim 8; Page 14; 21pp; English.

CC The present invention describes a high-affinity monoclonal antibody  
 CC characterised by an acid-washed enzyme-linked immunosorbent assay (EIA).  
 CC The antibody is used in cancer therapy. Association of the new antibody  
 CC with an antigen is favoured over dissociation in vivo and they therefore  
 CC have longer localisation times at target sites, resulting in a higher  
 CC concentration of antibodies localised at the target sites. Targeting the  
 CC antibody to a site in vivo is improved. The concentration of antibody  
 CC does not need to be too high which reduces side-effects and costs of  
 CC therapy. The present sequence represents the heavy chain variable region  
 CC of a monoclonal antibody having affinity for carcinoembryonic antigen  
 CC (CEA), a tumour associated antigen, which is used in the exemplification  
 CC of the present invention.

XX Sequence 121 AA;  
 XX

Query Match 100.0%; Score 614; DB 21; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-49;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQESGP<sub>1</sub>SLV<sub>2</sub>VP<sub>3</sub>SO<sub>4</sub>TL<sub>5</sub>ITCTV<sub>6</sub>SG<sub>7</sub>SLTK<sub>8</sub>YGV<sub>9</sub>SW<sub>10</sub>RQAP<sub>11</sub>KAL<sub>12</sub>EW<sub>13</sub>LG<sub>14</sub>VSS<sub>15</sub>GAL<sub>16</sub>TAY<sub>17</sub>N 60  
 |||  
 Db 1 qvqlqesgpslv<sub>1</sub>vp<sub>2</sub>spq<sub>3</sub>tl<sub>4</sub>stl<sub>5</sub>ctv<sub>6</sub>sg<sub>7</sub>sltk<sub>8</sub>ygv<sub>9</sub>sw<sub>10</sub>rgap<sub>11</sub>kale<sub>12</sub>w<sub>13</sub>lg<sub>14</sub>vss<sub>15</sub>gal<sub>16</sub>tay<sub>17</sub>n 60

QY 61 TALQSR<sub>1</sub>LSV<sub>2</sub>TRD<sub>3</sub>RSK<sub>4</sub>QSF<sub>5</sub>SLSS<sub>6</sub>VTTE<sub>7</sub>ED<sub>8</sub>PA<sub>9</sub>IY<sub>10</sub>CAK<sub>11</sub>SVNG<sub>12</sub>SD<sub>13</sub>VP<sub>14</sub>YGL<sub>15</sub>DW<sub>16</sub>SP<sub>17</sub>G<sub>18</sub>LL<sub>19</sub>TV<sub>20</sub>SS 120  
 |||  
 Db 61 talqsr<sub>1</sub>lsv<sub>2</sub>trd<sub>3</sub>rsk<sub>4</sub>qsf<sub>5</sub>slss<sub>6</sub>vtte<sub>7</sub>ed<sub>8</sub>pa<sub>9</sub>i<sub>10</sub>y<sub>11</sub>ca<sub>12</sub>k<sub>13</sub>sv<sub>14</sub>ng<sub>15</sub>sd<sub>16</sub>vp<sub>17</sub>ygl<sub>18</sub>d<sub>19</sub>w<sub>20</sub>sp<sub>21</sub>g<sub>22</sub>ll<sub>23</sub>tv<sub>24</sub>ss 120

QY 121 s 121  
 |||  
 Db 121 s 121

RESULT 2  
 AAR42796  
 ID AAR42796 standard; protein; 137 AA.  
 XX  
 AC AAR42796;  
 XX  
 DT 28-APR-1994 (first entry)  
 XX  
 DE Partial B4 Ab variable heavy chain.  
 XX  
 KW Monoclonal antibody; mAb; light: heavy; chain: variable;  
 KW complementarity determining region; CDR; B4; B13/B14; RSV19;  
 KW respiratory syncytial virus; RSV; F protein; antigen.  
 XX  
 OS Bos taurus.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT /label= CDR  
 FT 50..65  
 FT /label= CDR  
 FT Region 98..118  
 FT /label= CDR  
 FT Misc-difference 3  
 FT /note= "residue not defined in the specification"  
 XX  
 XX  
 PN WO9320210-A.  
 XX  
 PD 14-OCT-1993.  
 XX  
 PF 06-APR-1993; 93MO-GB00725.  
 XX  
 PR 06-APR-1992; 92GB-0007479.  
 XX  
 PA (SCOT-) SCOTGEN LTD.  
 XX  
 PI Stott EJ, Taylor G;  
 XX

DR WPI, 1993-336917/42.  
 XX  
 PT New antibodies against respiratory syncytial virus - including  
 PT humanised and chimeric antibodies, useful for treatment,  
 PT prevention and diagnosis of infection  
 XX  
 PS Disclosure: Fig 4; 139pp; English.  
 XX  
 CC Variable light chain and variable heavy chain sequences derived from  
 CC bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14  
 CC (AAR42794-R42797), and murine anti-RSV F protein mAb RSV19  
 CC (AAQ9376-049377), and their CDR peptides, may be used in the design of  
 CC fusion proteins (including altered antibodies) which are characterised by  
 CC the antigen binding specificity of these mAbs (for humanised Abs, see  
 CC AAR42798-R42801 and AAR42805-R42808).  
 CC NB: the specification is incomplete and published without claims.  
 XX  
 XX

Sequence 137 AA;  
 SQ

Query Match 70.0%; Score 430; DB 14; Length 137;  
 Best Local Similarity 67.4%; Pred. No. 3.5e-32;  
 Matches 87; Conservative 10; Mismatches 24; Indels 8; Gaps 1;

QY 1 QVQLQESGP<sub>1</sub>SLV<sub>2</sub>VP<sub>3</sub>SO<sub>4</sub>TL<sub>5</sub>ITCTV<sub>6</sub>SG<sub>7</sub>SLTK<sub>8</sub>YGV<sub>9</sub>SW<sub>10</sub>RQAP<sub>11</sub>KAL<sub>12</sub>EW<sub>13</sub>LG<sub>14</sub>VSS<sub>15</sub>GAL<sub>16</sub>TAY<sub>17</sub>N 60  
 |||  
 Db 1 qvqlqesgpslv<sub>1</sub>vp<sub>2</sub>spq<sub>3</sub>tl<sub>4</sub>stl<sub>5</sub>ctv<sub>6</sub>sg<sub>7</sub>sltk<sub>8</sub>ygv<sub>9</sub>sw<sub>10</sub>rgap<sub>11</sub>kale<sub>12</sub>w<sub>13</sub>lg<sub>14</sub>vss<sub>15</sub>gal<sub>16</sub>tay<sub>17</sub>n 60

QY 61 TALQSR<sub>1</sub>LSV<sub>2</sub>TRD<sub>3</sub>RSK<sub>4</sub>QSF<sub>5</sub>SLSS<sub>6</sub>VTTE<sub>7</sub>ED<sub>8</sub>PA<sub>9</sub>IY<sub>10</sub>CAK<sub>11</sub>SVNG<sub>12</sub>SD<sub>13</sub>VP<sub>14</sub>YGL<sub>15</sub>DW<sub>16</sub>SP<sub>17</sub>G<sub>18</sub>LL<sub>19</sub>TV<sub>20</sub>SS 112  
 |||  
 Db 61 talqsr<sub>1</sub>lsv<sub>2</sub>trd<sub>3</sub>rsk<sub>4</sub>qsf<sub>5</sub>slss<sub>6</sub>vtte<sub>7</sub>ed<sub>8</sub>pa<sub>9</sub>i<sub>10</sub>y<sub>11</sub>ca<sub>12</sub>k<sub>13</sub>sv<sub>14</sub>ng<sub>15</sub>sd<sub>16</sub>vp<sub>17</sub>ygl<sub>18</sub>d<sub>19</sub>w<sub>20</sub>sp<sub>21</sub>g<sub>22</sub>ll<sub>23</sub>tv<sub>24</sub>ss 120

QY 113 PGLLT<sub>1</sub>VSS 121  
 |||  
 Db 121 qgl<sub>1</sub>ltv<sub>2</sub>ss 129

RESULT 3  
 AAG66523  
 ID AAG66523 standard; Protein; 142 AA.  
 XX  
 AC AAG66523;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Humanised anti-CTLA4 heavy chain.  
 XX  
 KW Human: CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;  
 KW immunosuppressive; immunomodulator; anti-allelic; vaccine; antibody;  
 KW T cell; humanised antibody; autoimmune disorder; graft rejection;  
 KW allergy; heavy chain.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Synthetic.  
 XX  
 PN WO200154732-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001MO-US02653.  
 XX  
 PR 27-JAN-2000; 2000US-0178473.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;  
 PI O'Hara D, Hinton P, Tsunashita N;  
 XX  
 DR WPI; 2001-483195/52.  
 DR N-PSDB; AAR76441, AAR76443.  
 XX  
 PT Novel antibody-toxic group conjugate comprising an antibody that

Query Match	67.9%	Score 417	DB 22	Length 142
Best Local Similarity	66.7%	Pred. No. 5.8e-31		
Matches 82	Conservative 13	Mismatches 26	Indels 2	Gaps 1

OY	1	OVQLQESPPSLVAKFSQRLTSLCTVSGSGLKRYGVNWRQAAPGKLLEWLGCVSSALATAYN	60
Dd	20	qvqlqesgpgjlvpspqslstlctcvgsfsltsaygyvwrppgkglewlgvtawgtitgn	79
OY	61	TALDSRLSTRTDTSKSOFSLSSVTTEPRATYYCAKSVNGDSVP--YGIDWSPGILLT	118
		: : : : : : : : : : :	
Dd	80	salmrltltstckngysklssvtcaadclavyycatrgpphammkryamdyangvgtlvt	139
OY	119	VSS	121
Dd	140	VSS	142

RESULT	4
AAV22432	
ID	AAV22432 standard; protein; 120 AA

DT 28-SEP-1999 (first entry)

DE TM27 antibody VH chain mutant V67L, T68S, M69I, L70S, T73N.

KM IgG antibody; TM27; variable chain; immunoglobulin G; medical therapy  
 KN autoimmune disease; multiple sclerosis; antibody storage; VH; mutein;  
 KM heavy chain.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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98	98	98
99	99	99
100	100	100

/Label= V67L

ET /label= T685

ET /label= M69I

FT /label= L70S

FT /label= T73N

PN W09937329-A1.

XX	29-JUL-1999.	
PD		
XX		
PF	15-JAN-1999;	99WO-SE00049.

PR	09-MAR-1998;	98SE-0000766.
PR	22-JAN-1998;	98SE-0000170.

PA (ASTR ) ASTRA AB.

PI Flink O, Petren S;

DR WPI; 1999-458611/38.

PT Isotonic pharmaceutical formulations comprising a citrate

PS Claim 12; Page 23-24; 30pp; English.

CC This sequence is a mutant of the variable heavy (VH) chain of the  
CC antibody TW27. TW27 is an immunoglobulin G (IgG) antibody, contained in  
CC the isotonic pharmaceutical formulation of the invention, along with a  
CC citrate buffer at a physiologically acceptable pH. The formulations are  
CC useful in medical therapy, especially for treatment of autoimmune  
CC disease, and particularly, therapy of multiple sclerosis (using the TW27  
CC antibody heavy or light chains). The formulation is useful for improving  
CC the storage of an antibody. The antibody formulations are simple and  
CC effective. The formulations are stable and have improved storage  
CC properties. The formulation is simpler than prior art formulations.  
CC Existing antibody formulations require the use both of a stabiliser and a  
CC buffer. The present invention formulations are stabilized only by citrate  
CC buffer in a saline solution at a physiologically preferable pH. The  
CC avoidance of low pH prevents undesirable reaction at the site of  
CC injection. The formulation does not use ovalbumin for stabilisation,  
CC hence avoiding an allergic response to ovalbumin. Also the formulation  
CC does not require lyophilisation which is an expensive process and also  
CC requires the formulation to be resuspended prior to administration.

**SQ Sequence 120 AA**

Query Match	67.0%;	Score 411.5;	DB 20;	Length 120;
Best Local Similarity	66.1%;	Pred. No. 1.5e-30;		
Matches	82;	Conservative 14;	Mismatches 21;	Indels 7;
				Gaps 2

QY 1 QVQLQESGP<sub>SL</sub>VKPSQTLSLTCTVSGFSLTKYGVSWVRQAPGKALEWLGCVSSGALTAYN 600

Db 1 qvqlqesgpglvrpsqtlstctvsgfsltaygvnwvrqpprglewlgmhwgdgntdyn 600

61 TALQSRSLVTRDTSKSQFSLSLSSVTTEDTAIYYCAKSVNGDSVP---YGLDYWSPGLL 117

Db 61 saiksrlsiskdnknqfslrlssvtaadtavyycar---drvtatl YamdywgqgsLv 116

QY 118 TVSS 121

Db 117 tvss 120

RESULT	5
AAR42798	
ID	AAR42798 standard; protein; 129 AA

AC AAR42798 ;

DT 28-APR-1994 (first entry)

DE B4 HU-VH.

KW Monoclonal antibody; mAb; light; heavy; chain; variable;

KW respiratory syncytial virus; RSV; F protein; antigen

OS Chimeric: Bos taurus

```

OS Chimeric: Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /Label= CDR
FT Region 50..65
FT /Label= CDR
FT Region 98..118
FT /Label= CDR
XX
PN WO9320210-A.
XX
PD 14-OCT-1993.
XX
PF 06-APR-1993; 93WO-GB00725.
XX
PR 06-APR-1992; 92GB-0007479.
XX
PA (SCOT-) SCOTGEN LTD.
XX
PI Stott EJ, Taylor G;
XX
DR WPI, 1993-336917/42.
XX
PT New antibodies against respiratory syncytial virus - including
PT humanised and chimeric antibodies, useful for treatment,
PT prevention and diagnosis of infection
XX
PS Disclosure: Fig 10; 139pp; English.
XX
CC Variable light chain and variable heavy chain sequences derived from
CC bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14
CC (AA42794-R42797), and murine anti-RSV F protein mAb RSV19
CC (AA49376-049377), and their CDR peptides, may be used in the design of
CC fusion proteins (including altered antibodies) which are characterised by
CC the antigen binding specificity of these mAbs (for humanised Abs, see
CC AA42798-R42801 and AA42805-R42808).
CC NB: the specification is incomplete and published without claims.
CC
XX Sequence 129 AA:
SQ
Query Match 66.9%; Score 411; DB 14; Length 129;
Best Local Similarity 63.6%; Pred. No. 1.8e-30;
Matches 82; Conservative 13; Mismatches 26; Indels 8; Gaps 1;
QY 1 QVQLQESGPSTLVKPSQGLTSLCTFVSGFSLTKYGVSWVRQAPGKALEMIGVSSGALTAYN 60
DB 1 GYQLGESGPGILVRPESGLTSLCTVSGFSLTSYSVSWVRPQPGIQLGLDASNGILYYN 60
QY 61 TAIQSRSLVTRDTSKSQESLSLSSTTEPTAIYYCAKSVNGDSVPYG-----LDYWS 112
DB 61 palksvtrtlrtdtsknqfslrlssvtaadtavycakscvgsdysgacgkrgeydvavg 120
QY 113 PGLLTUVSS 121
DB 121 ggltlvss 129
XX
RESULT 6
AAW30273
ID AAW30273 standard; Protein; 137 AA.
XX
AC AAW30273;
XX
DT 07-JUL-1998 (first entry)
XX
DE Heavy chain of Hum4TS.22.
XX
XX Hum4TS.22: antibody; platelet derived growth beta receptor; PDGF-R beta;
KM inhibition; intimal hyperplasia; vasculature; restenosis; angioplasty;
XX heavy chain.
XX

```

```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 58..137
FT /note= "Mature Protein"
FT Binding-site 49..54
FT /note= "Complementarity determining region 1"
FT Binding-site 68..84
FT /note= "Complementarity determining region 2"
FT Binding-site 116..126
FT /note= "Complementarity determining region 3"
FT Misc-difference 20 /note= "Optionally Asn at position 1 of mature protein"
FT Misc-difference 49 /note= "Optionally Ser at position 30 of the mature protein"
FT Misc-difference 56 /note= "Optionally Ser at position 37 of the mature protein"
FT Misc-difference 66 /note= "Optionally Ile at position 48 of the mature protein"
FT Misc-difference 86 /note= "Optionally Ile at position 67 of the mature protein"
FT Misc-difference 92 /note= "Optionally Val at position 73 of the mature protein"
FT Misc-difference 93 /note= "Optionally Leu, Ile, and Met at position 74 of the mature protein"
FT Misc-difference 102 /note= "Optionally Ile at position 74 of the mature protein"102
XX
PN WO9737029-A1.
XX
PD 09-OCT-1997.
XX
PF 19-MAR-1997; 97WO-US04198.
XX
PR 22-MAR-1996; 96US-0621751.
XX
PA (BOE ) BOEHRINGER MANNHEIM GMBH.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Chang CN, Landolfi NF, Martin U;
XX
DR WPI, 1997-503114/46.
XX N-PSDB; AAT90980.
XX
PT Antibodies to platelet derived growth factor beta receptor - inhibit
PT PDGF BB-induced proliferation of cells expressing the receptor, used
PT particularly for inhibiting intimal hyperplasia
XX
PS Claim 6; Fig 2C; 87pp; English.
XX
XX This is the amino acid sequence for the heavy chain of Hum4TS.22, a
XX novel antibody which specifically binds to the platelet derived
XX growth beta receptor (PDGF-R beta), but not within the fifth
XX extracellular Ig-like domain, where the antibody inhibits PDGF
XX BB-induced proliferation of a cell expressing the PDGF beta receptor.
XX The antibody can be used in a method of inhibiting intimal hyperplasia
XX in the vasculature of a mammal. The antibodies can be used for the
XX treatment of disorders related to PDGF activity such as disorders
XX involving proliferation of smooth muscle cells, and including
XX restenosis following angioplasty.
XX
XX Sequence 137 AA:
SQ
Query Match 66.7%; Score 409.5; DB 18; Length 137;

```





[illegible][illegible]

```

FH Key Location/Qualifiers
FT Domain 1..116
FT /label= Variable_domain
FT Region 31..35
FT /label= CDR1
FT Region 50..65
FT /label= CDR2
FT Region 98..105
FT /label= CDR3
FT Domain 117..214
FT /label= CH1
FT Domain 215..234
FT /label= Hinge
FT Domain 235..273
FT /label= Fos_leucine zipper
FT Domain 340..446
FT /label= CH3

XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Glingrich R, Link BK, Tso JY, Weiner G;
XX
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Claim 28; Fig 4d; 85pp; English.
XX
XX The humanised ID10 antibody heavy chain (AAW05829) includes a
XX variable region (see also AAW05823) consisting of human R3.SHC heavy
XX chain variable region framework and complementarily determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 light chain (see also AAW05828) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX appls.
XX
XX Sequence 273 AA:

Query Match 65.9%; Score 404.5; DB 17; Length 273;
Best Local Similarity 64.5%; Pred. No. 1.7e-29;
Matches 78; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

OY 1 OVOLOEGSPSLVKGPSQTLSTLCTVSGFSLTKYGVSVWRQAPGKALEMLGCVSGALTAYN 60
DB 1 qyqlqesggjlykpseltlctctvgfsltnygvhvirpspgkglewlyvkwsqgstejn 60
OY 61 TALQSRSLVTRPTSKSQSFSLSVTTEDTAIYCAKSVNGDSVPYGLDYWSPGLLLTVS 120
DB 61 aefisrltskdstksqyvalkinsltaadctavyacardr-----yamdywsgqtlvtvs 115
OY 121 S 121
DB 116 s 116
```

```

RESULT 11
AAW05829
ID AAW05829 standard; Protein: 446 AA.
XX
XX AAW05829;
XX
XX 27-JAN-1997 (first entry)
XX
XX Humanised ID10 antibody heavy chain.
XX
XX B-cell lymphoma; humanised antibody; bispecific antibody;
XX myeloma; leukaemia; hybridoma; monoclonal antibody.
XX
XX Chimeric Homo sapiens.
XX Chimeric Mus sp.
XX
XX Key Location/Qualifiers
XX Domain 1..116
XX /label= Variable_domain
XX Region 31..35
XX /label= CDR1
XX Region 50..65
XX /label= CDR2
XX Region 98..105
XX /label= CDR3
XX Domain 117..214
XX /label= CH1
XX Domain 215..229
XX /label= Hinge
XX Domain 230..339
XX /label= CH2
XX Domain 340..446
XX /label= CH3

XX
XX WO9626964-A1.
XX
XX 06-SEP-1996.
XX
XX 29-FEB-1996; 96WO-US02754.
XX
XX 01-MAR-1995; 95US-0397411.
XX
XX (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Glingrich R, Link BK, Tso JY, Weiner G;
XX
XX WPI; 1996-412742/41.
XX
XX New bispecific antibody reactive with both T or NK cells and
XX malignant B cells - also their humanised forms and hybridomas
XX producing them, useful for treating or preventing leukaemia,
XX lymphoma and myeloma
XX
XX Example 4; Fig 4e; 85pp; English.
XX
XX The humanised ID10 antibody heavy chain (AAW05829) includes a
XX variable region (see also AAW05823) consisting of human R3.SHC heavy
XX chain variable region framework and complementarily determining
XX regions from the murine ID10 antibody specific for a 28/32 kDa
XX antigen found on the surface of malignant B-cells. It can be
XX coexpressed with humanised ID10 light chain (see also AAW05828) in
XX mammalian host cells. Bispecific antibodies can be constructed that
XX include a first binding fragment comprising humanised M291 heavy and
XX light chain variable regions (see also AAW05826, AAW05830), and a second
XX binding fragment comprising humanised ID10 heavy and light chain
XX variable regions. Such antibodies are reactive with both T or NK
XX cells and malignant B cells, and have therapeutic and diagnostic
XX appls.
XX
XX Sequence 446 AA:
```



CC the storage of an antibody. The antibody formulations are simple and effective. The formulations are stable and have improved storage properties. The formulations are simpler than prior art formulations. CC Existing antibody formulations require the use both of a stabiliser and a buffer. The present invention formulations are stabilised only by citrate CC buffer in a saline solution at a physiologically preferable pH. The CC avoidance of low pH prevents undesirable reaction as the site of CC infection. The formulation does not use ovalbumin for stabilisation, CC hence avoiding an allergic response to ovalbumin. Also the formulation CC does not require lyophilisation which is an expensive process and also CC requires the formulation to be resuspended prior to administration.

XX SQ Sequence 120 AA:

Query Match 64.1%; Score 393.5; DB 20; Length 120;

Best Local Similarity 63.7%; Pred. No. 6.9e-29;

Matches 79; Conservative 15; Mismatches 23; Indels 7; Gaps 2;

QY 1 QVQLQESGSLVSPQSLTCTVSGFSLTKYGVSWVROAPGKALEMIGVSSGALTAYN 60  
 DB 1 QVQLQESGPGYIVRPSGTLITCTVSGFSLTAYGVNWRVTPPGYGLWIGVIGDQNTDYN 60  
 QY 61 TALQSLRYTRDTSKSQFSLSSVTTEDTAIYYCAKSVNGDSVP---YGLDYWSPGLLL 117  
 DB 61 salksrvtmktsknqvfllrsvcaadtavycar----drvatllyamdywsggsly 116

OY 118 TVSS 121  
 DB 117 LVSS 120

RESULT 14

AAW22538  
 ID AAW22538 standard; Protein; 140 AA.

XX AAW22538;

XX 03-NOV-1997 (first entry)

DE Murine anti-human class II monoclonal antibody 44H104 VH chain.

XX Antibody; light chain; variable region; hybridoma cell line 44H104;  
 KW immune response; enhance; stimulate; vaccine; immunodiagnosis;  
 KM antigen delivery.

XX Mus musculus.

XX WO9640941-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-CA00400.

XX 07-JUN-1995; 95US-0483576.

XX (CONN-) CONNAGHT LAB LTD.

XX Anand NN, Barber BH, Caterini JE, Cates GC, Klein MR;

XX WPI: 1997-077271/07.  
 DR N-PSDB; AAT77852.

XX Recombinant conjugate antibody mol., modified for delivering an  
 PT antigen - elicits enhanced immune response without the use of  
 PT adjuvant to generate antibodies which are useful in vaccines or  
 PT immuno:diagnosis

XX Example 1; Fig 1B; 64pp; English.

XX Novel recombinant conjugate antibody molecules comprise a monoclonal  
 CC antibody specific for a surface structure of antigen presenting  
 CC cells (APC), genetically modified to contain at least one antigen

CC exclusively at one or more preselected sites. The conjugate is capable  
 CC of delivering the antigen to APC and eliciting an immune response to  
 CC the antigen. The new conjugates are useful as vaccines and are able  
 CC to elicit an enhanced immune response without the use of an adjuvant.  
 CC In a specific example, a conjugate was constructed using the murine  
 CC anti-human class II monoclonal antibody secreted by hybridoma  
 CC 44H104. The peptide C1B36 was chosen as antigen; it consists of  
 CC a tandemly linked T and B cell epitope derived from HIV MN strain.  
 CC The present sequence represents the heavy chain variable region  
 CC from 44H104 which was used in the preparation of a conjugate with  
 CC antigen C1B36.

XX SQ Sequence 140 AA:

Query Match 63.6%; Score 390.5; DB 18; Length 140;

Best Local Similarity 62.0%; Pred. No. 1.6e-28;

Matches 75; Conservative 17; Mismatches 28; Indels 1; Gaps 1;

QY 1 QVQLQESGPELVKPSQTLSTCTVSGFSLTKYGVSWVROAPGKALEMIGVSSGALTAYN 60  
 DB 21 QVQLKEGPGYIVAPSGSLITCTVSGFSLTSYGVNWRVTPPGYGLWIGVIGDQNTDYN 80  
 QY 61 TALQSLRYTRDTSKSQFSLSSVTTEDTAIYYCAKSVNGDSVPYGLDYWSPGLLLTVS 120  
 DB 81 salmsrlslskdnfksgvfkmslqvdtdtamyccaray\_gdyvhyamdywsggslytas 139

OY 121 S 121  
 DB 140 s 140

RESULT 15

AA42797  
 ID AA42797 standard; Protein; 141 AA.

XX AA42797;

XX 28-APR-1994 (first entry)

DE Partial B13/B14 Ab variable heavy chain.

XX Monoclonal antibody; mAb; light; heavy; chain; variable;  
 KW complementarity determining region; CDR; B4; B13/B14; RSV19;  
 KM respiratory syncytial virus; RSV; F protein; antigen.

XX Bos taurus.

XX Location/Qualifiers

XX Key 31..35

XX Region /label= CDR

XX Region 50..65

XX Region /label= CDR

XX Region 98..122

XX Region /label= CDR

XX Misc-difference 3

XX /note= "residue not defined in the specification"

XX /note= "residue not defined in the specification"

XX W09320210-A.

XX 14-OCT-1993.

XX 06-APR-1993; 93WO-GB00725.  
 XX 06-APR-1992; 92GB-0007479.  
 XX (SCOT-) SCOTGEN LTD.  
 XX Stott EJ, Taylor G;  
 XX WPI: 1993-336917/42.

XX New antibodies against respiratory syncytial virus - including  
PT humanised and chimeric antibodies, useful for treatment,  
PT prevention and diagnosis of infection

PS Disclosure; Fig 4; 139pp; English.

CC Variable light chain and variable heavy chain sequences derived from  
CC bovine anti-RSV F protein monoclonal antibodies (mAbs) B4 and B13/B14  
CC (AAR42794-R42797), and murine anti-RSV F protein mAb RSV19  
CC (AAR49376-Q49377), and their CDR peptides, may be used in the design of  
CC fusion proteins (including altered antibodies) which are characterised by  
CC the antigen binding specificity of these mAbs (for humanised Abs, see  
CC AAR42798-R42801 and AAR42805-R42808).

Sequence 141 AA;

Query Match	63.5%	Score	390	DB	14	Length	141
Best Local Similarity	63.4%	Pred. No.	1.7e-28				
Matches	85	Conservative	10	Mismatches	25	Indels	14
						Gaps	3

QY	1	QVQLQESPPSLPVKPSQSLTSLCTCYSGSLIRKYGVNWRKAPGKALEWIGGVSSGSGALTA	60
QY	1		61
QY	1		62
QY	1		63
QY	1		64
QY	1		65
QY	1		66
QY	1		67
QY	1		68
QY	1		69
QY	1		70
QY	1		71
QY	1		72
QY	1		73
QY	1		74
QY	1		75
QY	1		76
QY	1		77
QY	1		78
QY	1		79
QY	1		80
QY	1		81
QY	1		82
QY	1		83
QY	1		84
QY	1		85
QY	1		86
QY	1		87
QY	1		88
QY	1		89
QY	1		90
QY	1		91
QY	1		92
QY	1		93
QY	1		94
QY	1		95
QY	1		96
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QY	1		98
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QY	1		102
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QY	1		107
QY	1		108
QY	1		109
QY	1		110
QY	1		111
QY	1		112
QY	1		113
QY	1		114
QY	1		115
QY	1		116
QY	1		117
QY	1		118
QY	1		119
QY	1		120
QY	1		121
QY	1		122
QY	1		123
QY	1		124
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QY	1		126
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QY	1		146
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QY	1		148
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QY	1		167
QY	1		168
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QY	1		170
QY	1		171
QY	1		172
QY	1		173
QY	1		174
QY	1		175
QY	1		176
QY	1		177
QY	1		178
QY	1		179
QY	1		

Search completed: August 12, 2002, 09:25:38  
Job time: 168 sec









```
Ddb      19   OSVLTQPSPASGTPQOARVTICSCSGSSNIGSN-YYYWYQLPGTAPKLLIRNNRPSGV 77  
          | ||||| :|| :||||:::||:||||||| :||:  
  
Oy       61 PDREGSASSGNATLTLTISLSLAEDDADYCCASYOSTYG-VFGSSTRLVLG 111  
          |||||||| ::||:|||||||:| :|| ||||  
  
Db       78 PDRFSKSKSTGTSAISLAISGLRSDEADYCAAMDSDISGWVGGETKLTVLG 129  
  
RESULT  10  
         S25754  
Ig lambda chain - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000  
A:Accession: S25754  
R:Combrator, G.; Klobeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A>Title: V(Lambda) and J(Lambda)-CL(lambda) gene segments of the human immunoglobulin lam  
A:Reference number: SI6439; MUID:91257162  
A:Accession: S25754  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-235 <COM>  
A:Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA0956.1; PID:g33738  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:150-218/Domain: immunoglobulin homology<IMM>
```

```

Query Match          67.3%  Score 379.5; DB 2; Length 233;
Best Local Similarity 65.5%  Pred. No. 5.3e-24;
Matches 74; Conservative 17; Mismatches 19; Indels 3; Gaps 2;

QY 1 QDVLTPQSSVSGSLGQQRVITSCGSSSSNIGNAVYGMVQOVPGASAPRLILSATTEDRASGI 60
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 19 QSVLTQPSASGTPGQQRVITISCGSSSSNIGNT-VNWYQLPLGRAPKLLIHSNNRPSGV 77
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 PDRFSGSSGNTATLTITSSLOAEADADYCCASYSOSTVSG--VFSGSTRFLTVLG 111
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 78 PDRFSGSSGNTASALISGLSEDEADYCCAMDSDLNGRVYFGTGRVTVLG 130
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
S25752
I9 lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25752
R:Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(Lambda) and J(Lambda)-C(Lambda) gene segments of the human immunoglobulin lan
A:Reference number: S16439; MUID:91257162
A:Accession: S25752
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match          67.0%  Score 378; DB 2; Length 233;
Best Local Similarity 66.1%  Pred. No. 7e-24;
Matches 74; Conservative 16; Mismatches 20; Indels 2; Gaps 2;

QY 1 QDVLTPQSSVSGSLGQQRVITSCGSSSSNIGNAVYGMVQOVPGASAPRLILSATTEDRASGI 60
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 18 QSVLTQPSASGTPGQQRVITISCGSSSSNIGNT-VNWYQLPLGRAPKLLIHSNNRPSGV 76
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 61 PDRFSGSSGNTATLTITSSLOAEADADYCCASYSOSTVSG--VFSGSTRFLTVLG 111
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 77 PDRFSGSSGNTASALISGLSEDEADYCCAMDSDLNGRVYFGGCTKLTVLG 128
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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RESULT 12  
S29258  
Ig lambda chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jan-2000  
C:Accession: S29258  
R:Chouhan, L.; van Spriksen, A.; Breyer, J.; Guggenheim, P.; Strosberg, A.D.  
E:J. Biol. Chem. 207, 1115-1121, 1992  
A:Title: Molecular characterization of a human anti-Rh(D) antibody with a D(H) segmen  
A:Reference number: S29257; MUID:92362614  
A:Accession: S29258  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-216 <CHO>  
A:Note: only part of the coding sequence is given  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: pyrogutamic acid  
F:11-199/Domain: immunoglobulin homology <IM>  
F:1/Modified site: pyridone carboxylic acid (Gln) #status predicted

Query Match	66.8%	Score 377	DB 2	Length 216
Best Local Similarity	64.9%	Pred. No. 7.8e-24		
Matches	72	Conservative	16	Mismatches 23; Indels 0; Gaps 0.

[illegible]

```

RESULT 13
S51148
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51148
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi
A:Reference number: S51147
A:Accession: S51148
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <DEK>
A:Cross-references: EMBL:X83713
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
:13-90/Domain: immunoglobulin homology <IMM>

```

Query Match	66.8%;	Score 376.5;	DB 2;	Length 112;
Best Local Similarity	67.0%;	Pred. No. 4.6e-24;		
Matches 73; Conservative	16;	Mismatches 19;	Indels 1;	Gaps 1;

[illegible]

```
RESULT 14
SI6848
Ig lambda chain V-II region precursor - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S60297; SI6848
```

R:Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.

Immunol. Lett. 34, 57-62, 1992

A:Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm

A:Reference number: S60295; MUID:93122853

A:Accession: S60297

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KU2>

A:Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:34-111/Domain: Immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 66.7%; Score 376; DB 2; Length 136;  
Best Local Similarity 62.2%; Pred. No. 6e-24;

Matches 69; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

QY 1 QDVLQPPSSVSGSLGORVSTICGSSSNIGNAYVGMQVPGSAPRLISATTDRAST 60

DB 20 QSALRQPPSAGSPGOSVTISCTGTSDDGATNYSWYQHHPKAPKLMMEYSEKPSGV 79

QY 61 PDRFGSRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 111

DB 80 PDRFGSRSGNTATLTISLQAEDADYCCASYQSTYSGVFGSGTRLTVLG 130

#### RESULT 15

S25746

Ig lambda chain - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S25746

R:Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A:Reference number: S16439; MUID:91257162

A:Accession: S25746

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-236 <COM>

A:Cross-references: EMBL:X57811; NID:g33721; PIDN:CAA40948.1; PID:g33722

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:151-219/Domain: Immunoglobulin homology <IMM>

#### Query Match

Best Local Similarity 66.6%; Score 375.5; DB 2; Length 236;  
Best Local Similarity 64.3%; Pred. No. 1.1e-23;

Matches 72; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

QY 1 QDVLQPPSSVSGSLGORVSTICGSSSNIGNAYVGMQVPGSAPRLISATTDRAST 60

DB 20 QSVLRQPPSPVSGAPGOKITISGSSNIGAGHVMYQVPGTAPKLLIYADNNRPSGV 79

QY 61 PDRFGSRSGNTATLTISLQAEDADYCCASYQSTYSG-VFGSGTRLTVLG 111

DB 80 PDRISGSKGTASALITGLRADEADYCCQSPDSSLSCGVFGATKTLTVLG 131

Search completed: August 12, 2002, 09:23:27

Job time: 37 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 09:23:49 ; Search time 15.82 Seconds

(without alignments)  
271.673 Million cell updates/sec

Title: US-09-786-015-4

Perfect score: 564  
Sequence: 1 QDVLTPSSVSSLSGGRVSI.....SYGSTYSGVGSGTRRLTVLG 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	69.3	111	1	LV2H_HUMAN
2	382	67.7	111	1	LV2F_HUMAN
3	381	67.6	111	1	LV2C_HUMAN
4	373	66.1	109	1	LV2E_HUMAN
5	371	65.8	130	1	LV1G_HUMAN
6	370	65.6	111	1	LV2D_HUMAN
7	369	65.4	111	1	LV2G_HUMAN
8	367.5	65.2	112	1	LV2K_HUMAN
9	366	64.9	111	1	LV2I_HUMAN
10	363	64.4	111	1	LV1D_HUMAN
11	354.5	62.9	112	1	LV1H_HUMAN
12	347.5	61.6	112	1	LV1B_HUMAN
13	347	61.5	111	1	LV2B_HUMAN
14	344	61.0	109	1	LV1I_HUMAN
15	342	60.6	111	1	LV1A_HUMAN
16	341	60.5	109	1	LV1F_HUMAN
17	340	60.3	111	1	LV2A_HUMAN
18	332	58.9	111	1	LV1C_HUMAN
19	331.5	58.8	110	1	LV2J_HUMAN
20	319	56.6	103	1	LV1E_HUMAN
21	314	55.7	111	1	LV2L_HUMAN
22	311	55.1	106	1	LV4A_HUMAN
23	309	54.8	111	1	LV6D_HUMAN
24	307.5	54.5	131	1	LV6E_HUMAN
25	306.5	54.3	112	1	LV6A_HUMAN
26	306	54.3	106	1	LV4B_HUMAN
27	305	54.1	111	1	LV6C_HUMAN
28	299	53.0	106	1	LV4E_HUMAN
29	298	52.8	107	1	LV4C_HUMAN
30	294	52.1	108	1	LV5A_HUMAN
31	292	51.8	108	1	LV3A_HUMAN
32	291	51.6	111	1	LV3B_HUMAN
33	280	49.6	106	1	LV4D_HUMAN

34	272.5	48.3	114	1	KV4A_HUMAN	P01625	homo	sapien
35	270	47.9	111	1	LV7A_HUMAN	P01720	homo	sapien
36	269.5	47.8	113	1	LV1_CHICK	P04210	gallus	gall
37	267.5	47.4	108	1	KV1M_HUMAN	P01605	homo	sapien
38	265.5	47.1	108	1	KV1O_HUMAN	P01607	homo	sapien
39	264.5	46.9	129	1	KV1W_HUMAN	P04431	homo	sapien
40	264	46.8	109	1	KV3E_HUMAN	P01623	homo	sapien
41	264	46.8	129	1	KV4A_MOUSE	P01680	mus	musculu
42	262	46.5	109	1	KV1T_HUMAN	P01612	homo	sapien
43	261.5	46.4	112	1	LV6B_HUMAN	P01722	homo	sapien
44	260	46.1	109	1	KV3D_HUMAN	P01622	homo	sapien
45	259	45.9	133	1	KV4B_HUMAN	P06313	homo	sapien

## ALIGNMENTS

RESULT	ID	LV2H_HUMAN	STANDARD;	PRT;	111 AA.
AC	P01711;	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DR	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig lambda chain V-II region VII.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	NCBI_TaxID=9606;				
RP	SEQUENCE.				
RX	MEDLINE=71215142; PubMed=5087637;				
RA	Ponstingl H., Hilschmann N.;				
RT	"Structural rule of antibodies. Complete primary structure of a				
RT	monoclonal immunoglobulin L chain of the lambda type, subgroup II				
RL	(Bence Jones' protein VIL)."				
CC	-1- MISCELLANEOUS; THIS IS A BENCE-JONES PROTEIN.				
DR	PIR: A01977; L2HUVL.				
DR	HSP; P01709; 2MCG.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; Ig; 1.				
DR	SMART: SM00406; Ig; 1.				
KM	Immunoglobulin V region; Bence-Jones protein.				
FT	DISULFID 22 90				
FT	NON_TER 111				
SQ	SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;				
Query Match					
Best Local Similarity 69.3%; Score 391; DB 1; Length 111;					
Matches 73; Conservative 19; Mismatches 16; Indels 0; Gaps 0;					
OY	4	LVPPSSVSSLSGGRVSI	ITSGSSSSNIGNAVYGVQVPGSARLLISATTDRASGIPDR	63	
DB	4	LVQPAVSSLSGGRVSI	ITSGTSSDVGYNVSMFGHGTAKRLIIEVRNRPSSGSDR	63	
OY	64	FGSGRSNGTATLTITSSLAQDEADYVCASYOSTYSGVSGTRRLTVLG	111		
DB	64	FGSGRSNGTATLTITSSLAQDEADYVCASYOSTYSGVSGTRRLTVLG	111		
RESULT 2					
ID	LV2F_HUMAN	STANDARD;	PRT;	111 AA.	
AC	P01709;	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DR	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig lambda chain V-II region MGC.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=75013804; PubMed=4415202;  
RX MEDLINE=75013804; PubMed=4415202;  
RA Felt J.W., Deutsch H.F.;  
RT "Primary structure of the Mcg lambda chain."; Biochemistry 13:4102-4114(1974).  
RL [2]  
RN LAMBDA CHAIN GENES.  
RX MEDLINE=76093781; PubMed=812801;  
RA Felt J.W., Deutsch H.F.;  
RT "A new lambda-chain gene". Immunochimistry 12:643-652(1975).  
RL [3]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RA Edmundson A.B., Ely K.R., Aboia E.E., Schiffer M., Panagiotopoulos N.;  
RT "Rotational allomerism and divergent evolution of domains in immunoglobulin light chains."; Biochemistry 14:3953-3961(1975).  
RL [4]  
RN X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=90133913; PubMed=2515285;  
RA Ely K.R., Herron J.N., Harker M., Edmundson A.B.;  
RT "Three-dimensional structure of a light chain dimer crystallized in water. Conformational flexibility of a molecule in two crystal forms."; J. Mol. Biol. 210:601-615(1989).  
CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
CC -1- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY.  
CC SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.  
DR PIR: A01975; L2HUBC.  
DR PDB: 2MCG; 15-JUL-92.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IgV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT STRAND 3 5  
FT STRAND 10 12  
FT STRAND 18 23  
FT STRAND 26 32  
FT STRAND 36 40  
FT STRAND 42 43  
FT TURN 50 51  
FT STRAND 52 54  
FT TURN 55 55  
FT STRAND 62 63  
FT TURN 66 68  
FT STRAND 72 77  
FT STRAND 82 84  
FT HELIX 86 93  
FT STRAND 99 101  
FT STRAND 105 109  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11558 MW; 7CC1D6E2FA3377BA CRC64;

Query Match 67.7%; Score 382; DB 1; Length 111;  
Best Local Similarity 63.1%; Pred. No. 5,1e-31;  
Matches 70; Conservative 20; Mismatches 21; Indels 0; Gaps 0;  
OY 1 QDVLTPSPSSGSLGQVRSITCGSSSSNIGNANYGWOVPGSAPRLISATTTDRASGI 60  
DB 1 QSALTQPPSASGSLGQVRSITCGSSSDVGGYVSWYQOHGAKAPKVIITVEYKRPSSGV 60  
OY 61 PDRFGSGSGNATLTLSLQAEDEADYCCASYGRTYSGVFGSGRTLVLG 111

DB 61 PDRFGSGSGNATLTLSLQAEDEADYCCASYGRTYSGVFGSGRTLVLG 111  
RESULT 3  
ID LV2C\_HUMAN STANDARD; PRT; 111 AA.  
AC P01706;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region BOH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75115478; PubMed=804002;  
RA Kohler H., Rudofsky S., Klusens L.;  
RT "The primary structure of a human lambda II chain."; J. Immunol. 114:415-421(1975).  
RL [2]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE OZ+ MARKER.  
DR PIR: A01972; L2HUBH.  
DR HSSP: P01709; 2MCG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IgV; 1.  
KW Immunoglobulin V region.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11650 MW; 9452030932623E8 CRC64;

Query Match 67.6%; Score 381; DB 1; Length 111;  
Best Local Similarity 64.9%; Pred. No. 6.4e-31;  
Matches 72; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

OY 1 QDVLTPSPSSGSLGQVRSITCGSSSSNIGNANYGWOVPGSAPRLISATTTDRASGI 60  
DB 1 QSALTQPPSASGSLGQVRSITCGSSSDVGGYVSWYQOHGAKAPKVIITVEYKRPSSGV 60  
OY 61 PDRFGSGSGNATLTLSLQAEDEADYCCASYGRTYSGVFGSGRTLVLG 111  
DB 61 PDRFGSGSGNATLTLSLQAEDEADYCCASYGRTYSGVFGSGRTLVLG 111

RESULT 4  
ID LV2E\_HUMAN STANDARD; PRT; 109 AA.  
AC P01708;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region BOH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80006606; PubMed=113407;  
RA Infante A.J., Putnam F.W.;  
RT "Primary structure of a human IgA1 immunoglobulin V. Amino acid sequence of a human IgA lambda light chain (Bur)."; J. Biol. Chem. 254:9006-9016(1979).  
RL [2]  
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+ MARKERS.  
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR: A01974; L2HUBR.



RX MEDLINE-71103825; PubMed-5532228;  
 RA Wikler M., Putnam F.W.;  
 RT "Amino acid sequence of human lambda chains. 3. Tryptic peptides,  
 RT chymotryptic peptides, and sequence of protein Bo.";  
 RL J. Biol. Chem. 245:4488-4507(1970).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR: A01976; L2HUBO.  
 DR HSSP: P01709; 2MCG.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KM Immunoglobulin V region; Bence-Jones protein.  
 FT MOD\_RES 1  
 FT DISULFID 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT NON\_TER 111  
 FT SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 65.4%; Score 369; DB 1; Length 111;  
 Best Local Similarity 62.7%; Pred. No. 9.6e-30;  
 Matches 69; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

OY 1 QDVLTPSSVSGSLGQVRSITCGSSSNIGNAYGVQVGSAPRLISATTPDRASGI 60  
 DB 1 QSALTQPPASVSGPGOSVITISCTGTSVDGNKYVSWYQDHPKRAKLVFEVSQRPSCV 60  
 OY 61 PDFFSGSRSGNTATLTLSLQAEDEADYCCASYOSTYSGVSGTRLVIG 110  
 DB 61 PDFFSGSKSANTASLTLSLQAEDEADYCCSYVDNNNPFSGGTRLVIG 110

RESULT 8  
 LV2K\_HUMAN STANDARD; PRT; 112 AA.  
 AC P04209;  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-II region NIG-84.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-85204383; PubMed-3922791;  
 RX Tonioke H., Kametani F., Hoshi A., Shinoda T., Isobe T.;  
 RT "Amino acid sequence of an amyloidogenic Bence Jones protein in  
 RT myeloma-associated systemic amyloidosis.";  
 RL FEBS Lett. 185:139-141(1985).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN  
 CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.  
 DR PIR: A01971; L2HUNG.  
 DR HSSP: P01709; 2MCG.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KM Immunoglobulin V region; Amyloid; Bence-Jones protein.  
 FT DISULFID 22  
 FT NON\_TER 112  
 FT SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;

Query Match 65.2%; Score 367.5; DB 1; Length 112;  
 Best Local Similarity 63.4%; Pred. No. 1.4e-29;  
 Matches 71; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

OY 1 QDVLTPSSVSGSLGQVRSITCGSSSNIGNAYGVQVGSAPRLISATTPDRASGI 60  
 DB 1 QSALTQPPASVSGPGOSVITISCTGTSVDGNKYVSWYQDHPKRAKLVFEVSQRPSCV 60

OY 61 PDFFSGSRSGNTATLTLSLQAEDEADYCCASYOSTYSGVSGTRLVIG 111  
 DB 61 SNRFGSKSANTASLTLSLQAEDEADYCCSFTTNRAVGGGTRKLSVLG 112

RESULT 9  
 LV2L\_HUMAN STANDARD; PRT; 111 AA.  
 AC P01712;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-II region WIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-79062503; PubMed-102365;  
 RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;  
 RT "Amino acid sequence of the human myeloma lambda chain Win.";  
 RL Biochim. Biophys. Acta 537:9-21(1978).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR: A01978; L2HOWN.  
 DR HSSP: P01709; 2MCG.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KM Immunoglobulin V region; Bence-Jones protein.  
 FT MOD\_RES 1  
 FT DISULFID 22  
 FT NON\_TER 111  
 FT SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

Query Match 64.9%; Score 366; DB 1; Length 111;  
 Best Local Similarity 63.1%; Pred. No. 1.9e-29;  
 Matches 70; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

OY 1 QDVLTPSSVSGSLGQVRSITCGSSSNIGNAYGVQVGSAPRLISATTPDRASGI 60  
 DB 1 QSALTQPPASVSGPGOSVITISCTGTSVDGNKYVSWYQDHPKRAKLVFEVSQRPSCV 60  
 OY 61 PDFFSGSRSGNTATLTLSLQAEDEADYCCASYOSTYSGVSGTRLVIG 111  
 DB 61 PDFFSGSKSANTASLTLSLQAEDEADYCCSYGTRLVIG 111

RESULT 10  
 LV1D\_HUMAN STANDARD; PRT; 111 AA.  
 ID LV1D\_HUMAN  
 AC P01702;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-I region NIG-64.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-83186114; PubMed-6404900;  
 RA Kametani F., Takeyasu T., Suzuki S., Shinoda T., Okuyama T.,  
 RA Shimizu A.;  
 RT "Comparative studies on the structure of the light chains of human  
 RT immunoglobulins. IV. Assignment of a subgroup.";  
 RL J. Biochem. 93:421-429(1983).  
 DR PIR: A01965; L1HUNG.  
 DR HSSP: P01703; 7FAB.  
 DR InterPro: IPR003006; Ig\_MHC.



DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT MOD\_RES 1 1  
FT DISULFID 22 89  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 64.4%; Score 363; DB 1; Length 111;  
Best Local Similarity 65.2%; Pred. No. 3.7e-29;  
Matches 73; Conservative 15; Mismatches 22; Indels 2; Gaps 2;

OY 1 ODVLQPPSSVSGSLGQRYVITSCGSSSSNIGNAYGYQVQVGSAPRLISATFDRASGI 60  
DB 1 OSVLQPPSSVSAAPQOEYITSCGSSSSNIGDN-FVSWIQQLGTAPKRLITYNNKRPSGI 59  
OY 61 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVLG 111  
DB 60 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVLG 111

RESULT 11  
LV1B\_HUMAN STANDARD; PRT; 112 AA.  
AC P06887;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-I region MEM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=85257662; PubMed=2410269;  
RX Mhaesco E.; Roy J.P., Congy N., Peran-Rivat L., Mhaesco C.;  
RT "The amino acid sequence of a lambda light chain presenting abnormal  
physicochemical and antigenic features."  
RL Eur. J. Biochem. 150:349-357(1985).  
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES  
WERE POSITIONED BY HOMOLOGY.  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+  
MARKERS.  
DR PIR: A25479; LIHUM.  
DR HSSP: P01703; 7FAB.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Monoclonal antibody.  
FT MOD\_RES 1 1  
FT DISULFID 22 90  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFEB4 CRC64;

Query Match 62.9%; Score 354.5; DB 1; Length 112;  
Best Local Similarity 62.2%; Pred. No. 2.6e-28;  
Matches 69; Conservative 17; Mismatches 24; Indels 1; Gaps 1;

OY 1 ODVLQPPSSVSGSLGQRYVITSCGSSSSNIGNAYGYQVQVGSAPRLISATFDRASGI 60  
DB 1 OSVLQPPSSVSAAPQOEYITSCGSSSSNIGDN-FVSWIQQLGTAPKRLITYNNKRPSGI 60  
OY 61 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVL 110  
DB 61 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVL 111

RESULT 12

LV1B\_HUMAN STANDARD; PRT; 112 AA.  
ID LV1B\_HUMAN  
AC P01700;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-I region HA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71103824; PubMed=5532227;  
RA Shinoda T., Titani K., Putnam F.W.;  
RT "Amino acid sequence of human lambda chains. II. Chymotryptic  
peptides and sequence of protein Ha."  
RL J. Biol. Chem. 245:4475-4487(1970).  
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR: A01963; LIHUA.  
DR HSSP: P01703; 7FAB.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT MOD\_RES 1 1  
FT DISULFID 22 90  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Query Match 61.6%; Score 347.5; DB 1; Length 112;  
Best Local Similarity 63.1%; Pred. No. 1.3e-27;  
Matches 70; Conservative 16; Mismatches 24; Indels 1; Gaps 1;

OY 1 ODVLQPPSSVSGSLGQRYVITSCGSSSSNIGNAYGYQVQVGSAPRLISATFDRASGI 60  
DB 1 OSVLQPPSSVSAAPQOEYITSCGSSSSNIGDN-FVSWIQQLGTAPKRLITYNNKRPSGI 60  
OY 61 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVL 110  
DB 61 PDFFSGSRSGNTATLTITSLQADEADYVCASYQSYSG-VFGSGTRLTVL 111

RESULT 13  
LV2B\_HUMAN STANDARD; PRT; 111 AA.  
ID LV2B\_HUMAN  
AC P01705;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region NEI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=72233223; PubMed=5043326;  
RX Garver F.A., Hilschmann N.;  
RT "The primary structure of a monoclonal human lambda-type  
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI)."  
RL Eur. J. Biochem. 26:10-32(1972).  
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR: A01970; L2HUNI.  
DR HSSP: P01709; 2MCG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein.  
FT MOD\_RES 1 1  
SQ SEQUENCE 111 AA; 11789 MW; 748124F079CFEB4 CRC64;

FT DISULFID 22 90 BY SIMILARITY.  
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .).  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

Query Match 61.5%; Score 347; DB 1; Length 111;  
 Best Local Similarity 59.1%; Pred. No. 1.4e-27;  
 Matches 65; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

OY 1 OGVLPSPSVSGSLGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 60  
 1 QSVLTQPPSLAPGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 60  
 OY 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 110  
 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 110  
 DB 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 110

RESULT 14  
 ID LV11\_HUMAN STANDARD; PRT; 109 AA.  
 AC P06888;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-I region EPS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP MEDLINE=86000126; PubMed=3929803;  
 RA Toft K.G., Staeten K., Husby G.;  
 RT "The amino-acid sequence of the variable region of a carbohydrate-  
 containing amyloid fibril protein EPS (Immunoglobulin light chain,  
 RT type lambda).";  
 RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).  
 CC -1- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED  
 CC PEPTIDES WERE POSITIONED BY HOMOLOGY.  
 DR PIR: A24656; L1HUP.  
 DR HSP: P01703; 7FAB.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Amyloid; Glycoprotein.  
 FT CARBOHYD 104 104  
 FT DISULFID 22 89 N-LINKED (GLCNAC. . .).  
 FT NON\_TER 109 109 BY SIMILARITY.  
 SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match 61.0%; Score 344; DB 1; Length 109;  
 Best Local Similarity 64.0%; Pred. No. 2.7e-27;  
 Matches 71; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

OY 1 OGVLPSPSVSGSLGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 60  
 1 QSVLTQPPSLAPGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 59  
 DB 1 QSVLTQPPSLAPGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 59  
 OY 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111  
 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111  
 DB 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111

RESULT 15  
 ID LV1A\_HUMAN STANDARD; PRT; 111 AA.  
 AC P01699;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-I region VOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP MEDLINE=76023790; PubMed=809332;  
 RA Engelhard M., Hilschmann N.;  
 RT "Pattern of antibody structure. The amino acid sequence of a  
 RT monoclonal immunoglobulin L-chain of lambda-type, subgroup 1  
 RT origin of antibody specificity.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1413-1444(1975).  
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
 CC PIR: A01962; L1HVO.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT MOD\_RES 1 1 PYROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 22 89 BY SIMILARITY.  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 11514 MW; 21D9F64250DFC8E0 CRC64;

Query Match 60.6%; Score 342; DB 1; Length 111;  
 Best Local Similarity 59.8%; Pred. No. 4.3e-27;  
 Matches 67; Conservative 22; Mismatches 21; Indels 2; Gaps 2;

OY 1 OGVLPSPSVSGSLGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 60  
 1 QSVLTQPPSASGTPGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 59  
 DB 1 QSVLTQPPSASGTPGORSITCGSSSSNIGNANYGVQVGSAPRLISATTDASGI 59  
 OY 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111  
 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111  
 DB 61 PDFFSGSRSGNTATLTLSLQAEADYVCASYQSTYSGVFGSGTRLTVLG 111

Search completed: August 12, 2002, 09:23:49  
 Job time: 59 sec



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DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN  
DE VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal monoclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RL antibody V region genes.";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL: U96394; AAB68783.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 59.8%; Score 337.5; DB 4; Length 108;  
Best Local Similarity 65.7%; Pred. No. 1.4e-26;  
Matches 65; Conservative 14; Mismatches 19; Indels 1; Gaps 1;  
QY 1 QVLTQPPSSVSGSLGQVRSITCGSSSSNIGNAVYQVPGSAPRLISATTDRAAGI 60  
DB 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGSN-YVYVQQLPQTAKLLITRNQPSGV 59  
QY 61 PDRFSGSRGNATLTISSLOADEADYCYASTYSG 99  
DB 60 PDRFSGSKSTASLISGLRSEADYCYAAMDRLSG 98

RESULT 3  
Q96JD2 PRELIMINARY; PRT; 112 AA.  
AC Q96JD2;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perletti V., Casarini S., Colla Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region NEG.";  
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF267873; AAK58585.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match 57.1%; Score 322; DB 4; Length 112;  
Best Local Similarity 60.4%; Pred. No. 5.3e-25;  
Matches 67; Conservative 14; Mismatches 26; Indels 4; Gaps 3;  
QY 3 VLTQPPSSVSGSLGQVRSITCGSSSSNIGNAVYQVPGSAPRLISATTDRAAGI 62  
DB 3 MLTQPHSVSGSPGKTITICTSGSSGIASNS-VQWYQQRPGSAPNTVYENNRPGSVPD 61  
QY 63 RFSGS--RSGNTATLTISSLOADEADYCYASTYSGV-SGSTRLLTVLG 110  
DB 62 RFSGSIDSSNSASLITISGLKTEADYCYQSDSTNGVFGGKTLTVLG 112

RESULT 4  
Q96JD1

ID Q96JD1 PRELIMINARY; PRT; 112 AA.  
AC Q96JD1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perletti V., Casarini S., Colla Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region PIP.";  
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF267874; AAK58586.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 55.4%; Score 312.5; DB 4; Length 112;  
Best Local Similarity 58.6%; Pred. No. 4.8e-24;  
Matches 65; Conservative 14; Mismatches 29; Indels 3; Gaps 2;  
QY 3 VLTQPPSSVSGSLGQVRSITCGSSSSNIGNAVYQVPGSAPRLISATTDRAAGI 62  
DB 3 MLTQPHSVSGSPGKTITICTSGSSGIASN-YVQWYQQRPGSAPNTVYEDNRPGSVPD 61  
QY 63 RFSGS--RSGNTATLTISSLOADEADYCYASTYSGVFGGKTLTVLG 111  
DB 62 RFSGSIDSSNSASLITISGLKTEADYCYQSDSNNVALFGGKTLTVLG 112

RESULT 5  
Q96JD0 PRELIMINARY; PRT; 116 AA.  
AC Q96JD0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perletti V., Casarini S., Colla Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region SAR.";  
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF267875; AAK58587.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match 55.0%; Score 310; DB 4; Length 116;  
Best Local Similarity 59.8%; Pred. No. 8.9e-24;  
Matches 67; Conservative 13; Mismatches 28; Indels 4; Gaps 3;  
QY 3 VLTQPPSSVSGSLGQVRSITCGSSSSNIGNAVYQVPGSAPRLISATTDRAAGI 62  
DB 3 MLTQPHSVSGSPGKTITICTSGSSGIATN-YVQWYQQRPGSAPNTVYEDNRPGSVPD 61  
QY 63 RFSGS--RSGNTATLTISSLOADEADYCYASTYSGV-FSGSTRLLTVLG 111  
DB 62 RFSGSIDSSNSASLITISGLKTEADYCYQSDSISGNVIFGGKTLTVLG 113

RESULT 6  
Q96JD1

ID	Q9NSD6	PRELIMINARY:	PRT:	107 AA.
AC	Q9NSD6;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOTHETICAL PROTEIN (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LYMPHOCYTE.			
RA	Hohmann A.;			
RT	"Autoimmunity";			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; LA3092; AAA69746.2; -.			
DR	HSSP; P01709; ZMCG.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGV; 1.			
FT	NON_TER			
ET	NON_TER			
FT	107			
ET	107			
SEQUENCE	107 AA; 11306 MW; A2B04B37187A5F00 CRC64;			

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Query March      53.9%   Score 304; DB 4; Length 107;
Best Local Similarity 60.6%; Pred. NO.3.2e-23;
Matches 66; Conservative 9; Mismatches 30; Indels 4; Gaps 2
QY      4 LTPTPSVSGSLGQRYSITCSGSSSINGNNAVGMVQQVPGASAPRLILSATPTDRASGIPDR 63
        ||| ||| ||| ||| | : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2 LTQDPVSVALGQGVTRICQGDSLR---SYTASWVGQKRGQAPLYLTICKNNRPSGIDPR 58
OY      64 FSGSGSGATATTITISSLQAEDADYYCASYGTYS-GVFGSGTRLTVLG 111
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       59 FSGSSSGNTASTLTITGAQAEADADYYCNRSRDDSGNHAVFAGGTGLTVLG 107

RESULT 7
O9UL82
ID O9UL82 PRELIMINARY; PRT; 107 AA.
AC O9UL82;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
   (FRAGMENT).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56268.1; -.
DR HSSP; P01703; 7EAB.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
FT NON_TER 1
FT NON_TER 107
SEQUENCE 107 AA; 11445 MW; 52P0CC1AB26821DC CRC64;
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	Query Match	53.5%	Score 301.5	DB 4	Length 107
	Best Local Similarity	59.8%	Pred. No. 5,7e-23		
	Matches	64	Conservative	7	Mismatches 33; Indels 3; Gaps 1
Oy	4	LTPSPSVSGIGQRARITCSGSSSSNIGCAVYGVQVQVGPSPRLILSTTDBASGIPDR	63		
			:::		
	4	LTPSPSVSPQOTARITCSG--DLANKVVRWFQKQGAQPIILVFDTERPSGIPER	60		
Oy	64	FGSGSGMTATLTISLSLOAEDADYYCASYGTSYSGFSGRLTVL	110		
Db	61	FGSSSGTTVTLTISGAQVEDADYYCISASPNNGKRGEGGKLTLYL	107		

RESULT	8			
Q99M11				
ID	Q99M11	PRELIMINARY:	PRT:	235 AA.
AC	Q99M11;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOHETICAL 25.4 KDA PROTEIN.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_Taxid=10090;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC002129; AAH02129.1; -.			
DR	HSSP; P01703; 7FAB.			
DR	InterPro; IPR003559; Iq.			
DR	InterPro; IPR003597; Iq.cl.			
DR	InterPro; IPR003600; Iq.like.			
DR	InterPro; IPR003006; Iq.MHC.			
DR	InterPro; IPR003586; Iq.v.			
DR	Pfam; PF00047; Iq. 2.			
DR	SMART; SM00409; Iq. 2.			
DR	SMART; SM00407; Igcl. 1.			
DR	SMART; SM00406; Igv. 1.			
DR	SMART; SM00410; Ig.like. 2.			
DR	PROSITE; PS00290; Iq.MHC; UNKNOWN_1.			
DR	Hypothetical protein.			
Q0	SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;			

	Query Match	50.0%	Score 282;	DB 11;	Length 235;	
	Best Local Similarity	56.2%;	Pred.No. 1.4e-20;			
	Matches	63;	Conservative	12;	Mismatches 33;	Indels 4; Gaps 3
Oy	1 QDLVLPQSSVSLSLCORVITCGSSSNIGGNAYGVYQOVPGSAPRLILSATTDTRASGI 60                     :     :     :     :     :     :     :     :					
Dd	20 QLVLTPQSSVSYSLSGLSTALPCKASTGNI-GDSYVMWYQQIYMGKRSPTNNMITYGDLLRPSGY 78					
Oy	61 PDRESGS--RSGNTATLTTISLQAEDADNYCCASQYSTYSGVFGSGTRLLTV 110                     :     :     :     :     :     :     :     :					
Dd	79 SDRFSGSIDSSNSAFLTIQNVADDEADYCYOSYSSGIR-VFGGSKTLTVL 129					
RESULT	9					
O9UL77						
ID	O9UL77	PRELIMINARY:	PRT;	108 AA.		
AC	O9UL77:					
Dt	01-MAY-2000 (TREMBLrel. 13, Created)					
Dt	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
Dt	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).					
Dd	OS Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					

RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; PubMed=9614934;
RA	Wu X., Liu B., Van der Werpe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.,
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035037; AAD56273.1; -.
DR	HSSP; P01607; IREI.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00406; Igv_1.
FT	NON_TER 1
FT	NON_TER 108 108
SQ	SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match	47.48	Score 267.5	DB 4	Length 108
Best Local Similarity	55.18	Pred. No. 1.5e-19		
Matches 59, Conservative	12	Mismatches 31	Indels 5	Gaps 3

```

QY      63  RFGSGRGATATLTITSLDAEDADYYTCASTQSYTSGVFGSGRTLTIV 109
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61  RFGSGGDTFTLTITSLDPEFATYYCOQSYST-SWFGSGGTVEI 106
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT	10
096SA9	
ID	096SA9
AC	096SA9
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE	ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98375893; PubMed=9712075;
RA	Adedson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT	"Molecular analysis of polyreactive monoclonal antibodies from
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT	antibody V region genes.";
RL	J. Immunol. 161:2020-2031(1998).
DR	EMBL; U96396; AAB68765.1; -.
FT	NON_TER
FT	NON_TER
FT	NON_TER
SEQUENCE	107 AA; 11520 MW; 4BB4359C5B577F16 CRC64;

Query Match	47.3%	Score 267	DB 4	Length 107
Best Local Similarity	54.6%	Pred. No. 1.7e-19		
Matches 59	Conservative 15	Mismatches 26	Indels 8	Gaps 4

QY	63	RFGSGRGATATITISLDAEDADYYCASQVITYSGV-FESGRRLTV	109
	61	RFSGSGGDEFTLTISLQPEDFATYYC--QASVLTTFEGGKRVKI	105
Dd	4	MTQPSLSLAVSDRVITTCRASQSI--SSLTLMYQOKPEKARKLLIYAASLQSGVPS	60
QY	4	LTO-PSSVSSLSLQARYISITGSSSSNINIGMAVYQVQPSAPARLLISATTPRASIPD	62

RESULT  
Q9U410

ID	090410	PRELIMINARY;	PRT;	106 AA.
AD	090410:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MONOCLONAL ANTI-ID10TYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN			
DE	VARIABLE REGION (FRAGMENT).			
OS	Schistosoma japonicum (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida			
OC	Schistosomatoidea; Platyhelminthae; Schistosomidae.			
OX	NCBI_Taxid=6182;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Song X.T., Peng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;			
RT	"Amplification, cloning and sequence analysis of the light chain			
RT	variable region gene of monoclonal anti-Idiotypic antibody NP30 of			
RT	Schistosoma japonicum."			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF207620; AAF19434.1; -			
DR	HSSP; P01679; 2PBJ.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SMO0406; IGV; 1.			
FT	NON_TER	1		
FT	NON_TER	1		
FT	NON_TER	106	106	
SQ	SEQUENCE	106 AA;	11478 MW;	F20E544426BA6E3E CRC64;

Query Match	47.0%;	Score 265;	DB 5;	Length 106;
Best Local Similarity	53.7%;	Pred. No. 2.6e-19;		
Matches	58;	Conservative	20;	Mismatches 24;
			Indels	6;
			Gaps	3

Dy 60 I P D F S G S R G N T A I T T I S L O A E D E A D Y C A S I O S T V S G V F G S G I T L 107  
::: ||||| :::: |::| :::: |::| :::: |::| :::: |::| :::: |::| :::: |::| :::  
Db 57 V P A F S G S G S G T Y S L T I S R M A E A A A T Y C Q O W M T S - V P F F G S G I T L 103

RESULT	12	
Q9UL81		
ID	Q9UL81	PRELIMINARY; PRT; 107 AA.
AC	Q9UL81;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	WOSTIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
DE	Homo sapiens (Human).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.	
OX	NCBI_TaxID=9606;	



```

Query Match          46.8%; Score 264; DB 4; Length 107;
Best Local Similarity 54.6%; Pred. No. 3.3e-19;
Matches    59; Conservative   13; Mismatches   28; Indels    8; Gaps

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4

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OY      4 LTO-PSSVSGSLGQRVSTICSGSSSNNIGCNAVGWQVGSAPRLLIATTDRAAGIPD 62
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 MTQSPSSLASAGDRAVTITCRASGSI---SNLNMVQKRPGRAPNLLIYAASSLSQSVPS 60
OY      63 RFGSGRGNTATLTITSSLOADEADYYCASYSYSTSGV-FSGSTRITLV 109
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 RFGSGSGSDPFLTITSGLOAEDFATRYVC---QQSVALTFGGPKVKDI 105

```

RESULT 13

O96I69 PRELIMINARY; PRT; 233 AA.

O96I69

AC O96I69;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE UNKNOWN (PROTEIN FOR MGCI12849).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PRIMARY B-CELLS FROM TONSILS;

RA Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.

DR EMBL, BC007782, AAH07782.1, ..

SO SEQUENCE 233 AA; 24802 MW; C694E8397B27650B CRC64;

Query Match	46.1%	Score 260	DB 4	Length 233
Best Local Similarity	52.7%	Pred. No. 2.2e-18		
Matches 58	Conservative 16	Mismatches 32	Indels 4	Gaps 3

  

QY	3	VLTPOSSVSGSLGQRFVSTJTCSSGSSNIGGNAMVGVQVPGSAPRLISATYMDRASGLPD	62
Db	22	VLTQPSVSVAPAGCFARATTCGG-SNLDSKS-VNNYQLRPGCALPLVYENNERFAGIPE	78
QY	63	RFGSGRSGNTATLTSSLQADDEADLYTCASYST-YSGYFGSGTRLTVLG	111
Db	79	RLSALTSEETATLTSSVAGDEADYFCQVMDTTSQOQYVFGTQTVLGG	128

  

RESULT	14
Q9UL70	PRELIMINARY; PRT; 108 AA.
AC	Q9UL70.
DT	01-MAY-2000 (TREMBLrel. 13; Created)
DT	01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DE	01-DEC-2001 (TREMBLrel. 19; Last annotation update)
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_Taxid-9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-98277139; PubMed-9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035044; AAD56280.1; -.
DR	HSSP; P01607; IRET.
DR	InterPro; IPR003006; I9_MHC.
DR	InterPro; IPR003596; I9_V.

DR	Pfam, PF00047; Ig, 1.	
DR	SMART; SM00406; IgV, 1.	
FT	NON_TER	1
FT	NON_TER	108
SO	SEQUENCE	108 AA; 1163 MW; B7BEDC3FA1FCCA37 CRC64;

Query Match	46.0%	Pred. 259.5	DB 4	Length 108;
Best Local Similarity	53.3%	Pred. No. 9.6e-19;		
Matches 57; Conservative	11;	Mismatches 34;	Indels 5;	Gaps 3;

Db 61 RFSGSGGTDFLTISGLQAEDFATYYC---QQSYSALTGPGTKVDI 105

```
QY      4 LTQ--PSSVSGSLGQRVSLTSCGSSSNIGNAYGVWQQVPGSAPRLLIATITDRASGIPD 62Z
        :|||:::||::||| |   |::||| ||::||| |   |::|||
Db      4 MTQPSSLASAVGDRTYTTCRASQ--GISNYLAWYQKPKGYPKSLIYAASTLGSGVPS 600
```

```
QY      63 RFGSGSRGNTATLTITSSLQAEDEADYCCASYQSTYSGVFGSGTRLTV 109
      ||||| || ||||| || || || ||||| :
Db      61 RFGSGSGTDTFTLTITSSLQPEDVATYYCQKYNNSA-PRTEPGTKLEI 106
```

RESULT 15

ID	Q9ERZ9	PRELIMINARY;	PRT;	107	AA.
1	000000				

DT	01-MAR-2001 (Tremblay, last sequence update)
DI	01-MAR-2001 (Tremblay, 16, created)

DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FBAGMENT).  
DI 01-DEC-2001 (FIREBLTrel. 19, last annotation update)

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.

### RT "Cloning and sequencing of the light chain fragment of va

RL	J. Cell. Mol. Immunol. 12:21-26 (1996).
RN	[2]

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.,

human TNF-alpha specific monoclonal antibody."; RT

RN [3]

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.

DR EMBL; AF262753; AAG23804.1; -,  
DR HSSP: P80363; 1WTI

DR	InterPro: IPR003599; Ig.
DR	InterPro: IPR003006; Ig MHC

DR Pfam; PF00047; 1q; 1.

DR SMART; SM00406; IGV; 1.

SQ SEQUENCE 107 AA; 11784 MW

Quincy Match 4E 38.

Best Local Similarity 49.1%;  
Matches 53: Conservative 1

4 LTO-PSSVSGSLGORVSTCSGS

Db 1 MTQSPSSIAMSVGQKVTMSCKSS

QY 60 IPDRFSGSRGNTATLTISSLQA

Db 61. VPDREMGSGSGTDETLTISVQT

DR	Pfam; PF00047; 1g; 1.
DR	SMART; SM00406; IGV; 1.
FT	NON_TER 1 1
FT	NON_TER 108 108
SO	SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
Query Match	46.0%; Score 259.5; DB 4; Length 108;
Best Local Similarity	53.3%; Pred. No. 9.6e-19;
Matches 57; Conservative 11; Mismatches 34; Indels 5; Gaps 3.	
OY	4 LTQ-PSSVSGSLGQRYSTCGSSSSNIGGMAYGVGYQVPGPSAPRLLISATTDRAAGIRD 62 .:        . :         : : : :         : : : :         Db 4 TMSSTLSASAGDHYVTITCRASQ---GISNTLAWYQQKPKGVPSRLTYAAASTLAGSVPS 60
OY	63 PFGSRSRGNTATLTITSSLQAEDEARYCCASYGTYSVPGSGTRLTV 109                                     : :       : Db 61 PFGSGSGTDFTLTISSLPEDVATYYCKYNISA-PTTFGPETKETI 106
RESULT 15	
O9ERZ9	
ID O9ERZ9 PRELIMINARY; PRT; 107 AA.	
AC O9ERZ9:	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
DJ 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
CX NCBI_TaxID=10090;	
NN [1]	

[illegible]

Search completed: August 12, 2002, 09:24:41  
Job time: 111 sec

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A:Residues: 1-140 <DUF>  
A:Cross-references: EMBL:249175; NID:g794118; PIDN:CAA89044.1; PID:g794119  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 440; DB 2; Length 140;  
Best Local Similarity 71.9%; Pred. No. 4.5e-31;  
Matches 87; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVKPSQTLSTCTVSGFSLTKKYGVSWMVROAPGKALEWLGVSAGALTAYN 60  
|||||  
DB 20 QVQLQESGPELVKPSQTLSTCTVSGFSLTSNNVGMVROAPGKALEWVGDIYAGSKETYS 79  
OY 61 TALQSLRSLVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPYGLDYWSPGLLTYS 120  
||:|||||  
DB 80 PALKSRSLRTRDTSKQSVSLSSVTTEEDTAIVYVCARDQPSGVFGDYWDYWGPGLLVTYS 139  
OY 121 S 121  
DB 140 S 140

## RESULT 7

S54240  
Ig mu heavy chain V region precursor - sheep (fragment)

C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 23-Jul-1999  
C:Accession: S54240  
R:Dufour, V.; Nau, F.  
submitted to the EMBL Data Library, April 1995  
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.  
A:Reference number: S54225  
A:Accession: S54240  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <DUF>  
A:Cross-references: EMBL:249176; NID:g794120; PIDN:CAA89045.1; PID:g794121  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 439; DB 2; Length 140;  
Best Local Similarity 72.7%; Pred. No. 5.4e-31;  
Matches 88; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVKPSQTLSTCTVSGFSLTKKYGVSWMVROAPGKALEWLGVSAGALTAYN 60  
|||||  
DB 20 QVQLQESGPELVKPSQTLSTCTVSGFSLTSNNAVDWVRQAPKVPKPEMLGVSISGSTRYN 79  
OY 61 TALQSLRSLVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPYGLDYWSPGLLTYS 120  
||:|||||  
DB 80 PALKSRSLRTRDTSKQSVSLSSVTTEEDTAIVYVCARTWYSGCAGCSIDYWGPGLLVTYS 139  
OY 121 S 121  
DB 140 S 140

## RESULT 8

S54248  
Ig mu heavy chain V region precursor - sheep (fragment)

C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S54248  
R:Dufour, V.; Nau, F.  
submitted to the EMBL Data Library, April 1995  
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.  
A:Reference number: S54225  
A:Accession: S54248  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-140 <DUF>  
A:Cross-references: EMBL:249172; NID:g794137; PIDN:CAA89041.1; PID:g794138  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 439; DB 2; Length 140;  
Best Local Similarity 72.7%; Pred. No. 5.4e-31;  
Matches 88; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVKPSQTLSTCTVSGFSLTKKYGVSWMVROAPGKALEWLGVSAGALTAYN 60  
|||||  
DB 20 QVQLQESGPELVKPSQTLSTCTVSGFSLSDAVNVMVROAPGKALEWVGDIYAGSKETYS 79  
OY 61 TALQSLRSLVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPYGLDYWSPGLLTYS 120  
||:|||||  
DB 80 PALKSRSLRTRDTSKQSVSLSSVTTEEDTAIVYVSATCLYRSCHTNGHAYWSPGLLTYS 139  
OY 121 S 121  
DB 140 S 140

## RESULT 9

S54233  
Ig mu heavy chain V region precursor - sheep (fragment)

C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S54233  
R:Dufour, V.; Nau, F.  
submitted to the EMBL Data Library, April 1995  
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.  
A:Reference number: S54225  
A:Accession: S54233  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <DUF>  
A:Cross-references: EMBL:249165; NID:g794105; PIDN:CAA89034.1; PID:g794106  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
F:34-115/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 438.5; DB 2; Length 139;  
Best Local Similarity 71.9%; Pred. No. 6e-31;  
Matches 87; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

OY 1 QVQLQESGPELVKPSQTLSTCTVSGFSLTKKYGVSWMVROAPGKALEWLGVSAGALTAYN 60  
|||||  
DB 20 QVQLQESGPELVKPSQTLSTCTVSGFSLTSNNAVGMVROAPKVPKPEMLGVSISGSTRYN 78  
OY 61 TALQSLRSLVTRDTSKQSFSLSSVTTEEDTAIYYCAKSVNGDSVPYGLDYWSPGLLTYS 120  
||:|||||  
DB 79 PALKSRSLRTRDTSKQSVSLSSVTSEDTAIVYVCARAYGYLYCHHIDYWGPGLLVTYS 138  
OY 121 S 121  
DB 139 S 139

## RESULT 10

S54242  
Ig mu heavy chain V region precursor - sheep (fragment)

C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)  
C:Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S54242  
R:Dufour, V.; Nau, F.  
submitted to the EMBL Data Library, April 1995  
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.  
A:Reference number: S54225  
A:Accession: S54242

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <DUF>  
A:Cross-references: EMBL:Z49170; NID:g794125; PID:CAA89039.1; PID:g794126  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
F:3-4-116/DomaIn: immunoglobulin homology <IMM>

Query Match	71.38;	Score 438;	DB 2;	Length 140;
Best Local Similarity	69.48;	Pred. No. 6.6e-31;		
Matches	84;	Conservative	16;	Mismatches 21;
			Indels	0;
			Gaps	0;

QY	1	OYOLQESPSLYKPSQTLSTLCYTGSGSLTFKGYGWSYWRQAKRLTMDLGGVSSCALTAYN	60
Db	20	QYRLQESPSLYKPSQTLSTLCYTGSGSLTSMNAHWWRQAKRLEMDLGGVSSCALTAYN	79
QY	61	TALQSLRSLVTRDTSKQSPSLSSSVTTEDTAIYYCAKSVNGDSVPYGLDWSPELLLTVS	120
Db	80	PALMSRLSLTRDTSKQSVSLSSSVTSDDTAVYYCARDIDGTANWMDIETWGPPELLTVS	139
QY	121	S	121
Db	140	S	140

```

RESULT 11
S54226
ig mu heavy chain V region precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C:Accession: S54226
R:DuFour, V.; Nau, F.
Submitted to the EMBL Data Library, April 1995
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.
A:Reference number: S54225
A:Accession: S54226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <DUF>
A:Cross-references: EMBL:Z49158; NID:g794091; PIDN:CAAB8027.1; PID:g794092
C:Superfamily: Immunoglobulin V region; Immunoglobulin V region
C:Keywords: Immunoglobulin
/34-116/Domain: immunoglobulin homology <IMM>

```

Query Match	71.1%	Score 436.5	DB 2	Length 141
Best Local Similarity	71.3%	Pred. No. 9e-31		
Matches	87	Conservative	12	Mismatches 22; Indels 1; Gaps 1.
Qy	1	QVQLDSEGSLVLRKPSQTLISLTCTVSGSFILTKYGVSWRQAPKALEMLGAGVSSGALTAVN	60	
Db	20	QVQLDSEGSLVLRKPSQTLISLTCTVSGSFSSNNAVGWRQAPKLTLEWGNIMSDGSTIYN	79	
Qy	61	TALQSRLSVTRDTSKQPSLSLSVTTEDTALYYCAKSYN-GDSVYEGHLYWSPGLLITV	119	
Db	80	PALKSRLSITTRDTSKQPSLSLSVSIDDTALYYCARDENSQWITYGGIDYWGPGLLIYV	139	
Qy	120	SS 121		
Db	140	SS 141		

RESULT 12  
S54241  
Ig mu heavy chain V region precursor - sheep (fragment)  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 23-Jul-1999  
C/Accession: S54241  
R/Dutour, V.; Nau, F.  
submitted to the EMBL Data Library, April 1995  
A/Description: Sheep immunoglobulin mu heavy chain variable region sequence.  
#Reference number: S54225

A:Accession:SF54241  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-142 <DUF>  
A:Cross-references: EMBL:Z49177; NID:g794122; PIDD:CA89046.1; PIDD:g794123  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
E:34-116/Domain: immunoglobulin homology <IM>

Query Match	71.0%;	Score 436;	DB 2;	Length 142;
Best Local Similarity	70.6%;	Pred. No. 1e-30;		
Matches	89;	Conservative 12;	Mismatches 17;	Indels 8;
			Gaps	3

[illegible]

```

RESULT 13
S54246
1) mu heavy chain V region precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C:Accession: S54246
R:DuFour, V.; Nau, F.
Submitted to the EMBL Data Library, April 1995
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence
A:Reference number: S54225
A:Accession: S54246
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <DUF>
A:Cross-references: EMBL:Z49171; NID:g794133; PIDN:CAAB8040.1; PID:g794134
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 14  
S54231  
Igm heavy chain V region precursor - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 08-Jul-1995 #sequence 03-Aug-1995 #text\_change 23-Jul-1999  
C:Accession: S54231  
R:DuFour, V.; Nau, F.  
Submitted to the EMBL Data Library, April 1995  
A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.

A:Reference number: S54225  
A:Accession: S54231  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-139 <DUF>  
A:Cross-references: EMBL:Z49167; NID:g794101; PIDN:CAA89036.1; PID:g794102  
C:Superfamily: Immunoglobulin V region; Immunoglobulin Homology  
C:Keywords: Immunoglobulin  
C:34-116/Domain: Immunoglobulin homology <IMM>

Query Match	70.8%	Score 434.5	DB 2	Length 139
Best Local	69.4%	Pred. No. 1.3e-30		
Matches 84	Conservative 13	Mismatches 23	Indels 1	Gaps 1

```

0Y 1 QVOLOESPSPLYKRSQTSILCTCYSGLKRYGAWRROAKPKRLMLGLGVSQALATYAN 60
Db 20 QVOLOESPSPLYKRSQTSILCTCYSGLKRYGAWRROAKPKRLMLGVSITGSGCLATYN 79

0Y 61 TALOSRLSVYNDIRSKQSPSLSSLSVTTEDPRAIYYCAKSVNGDSVPYGLDWSFQLLTYS 120
Db 80 PALKSRSLITNDIRSKQSVSLSSLSVTTEDDAVYYCAR-ISSGGAAPSYIDWIGPELLATYS 138

```

QY	121	S	121
Db	139	S	139

```

RESULT      15
S54244
I:  mu heavy chain V region precursor - sheep (fragment)
C:  Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:  Date: 08-Jul-1995 #sequence #revision 03-Aug-1995 #text-change 23-Jul-1999
C:  Accession: S54244
R:  Dutoir, V.; Nau, F.
   Submitted to the EMBL Data Library, April 1995
A:  Description: Immunoglobulin mu heavy chain variable region sequence
A:  Reference number: S54225
A:  Accession: S54244
A:  Status: preliminary
A:  Molecule type: mRNA
A:  Residues: 1-144 <DUF>
A:  Cross-references: EMBL:Z49173, NID:G794129, PIRN:CAAB9042.1, PID:G794130
C:  Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:  Keywords: Immunoglobulin
C: 34-116/Domain: Immunoglobulin homology <IM>

```

Query Match	70.48;	Score 432;	DB 2;	Length 144;
Best Local Similarity	70.68;	Pred. No. 2.2e-30;		
Matches 89;	Conservative 11;	Mismatches 20;	Indels 6;	Gaps 2;

Qy 1 QVQLQESPPSLVYKRSQTLISLTCTAYSGSLRKYGVSWVRQAPGKRLIEWIGGVSSALTAAY 60  
Db 20 QVRLQESPPSLVYKRSQTLISLTCTAYSEPSLTITTYGVGWVRQAPGKRLIEWLSTIYNNQDTDYN 79  
Qy 61 TALQSRSLVTEPDTSKSQPSLSSVTEEDRAIYYCAASVAGDSVPY-----GLDYMSFGL 115  
Db 80 AALSKRSLITRDTSKSVSLSSVTEEDRAIYYCTRDTSKRS-GVANGIGVDVFWGRL 138  
Qy 116 LRVVSS 121  
Db 139 LRVVSS 144

Search completed: August 12, 2002, 09:23:26  
Job time: 36 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 09:22:50 ; Search time 15.82 Seconds

(without alignments)  
296.148 Million cell updates/sec

Title: US-09-786-015-2

Perfect score: 614  
Sequence: 1 QVQLQESGSLVSPQSLTL.....DSVPYGLDWSPGLLTVSS 121

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	59.9	144	1	HY43_MOUSE
2	351	57.2	137	1	HY46_MOUSE
3	338	55.0	116	1	HY45_MOUSE
4	336	54.7	115	1	HY44_MOUSE
5	334.5	54.5	146	1	HY21_HUMAN
6	331.5	54.0	116	1	HY61_MOUSE
7	327	53.3	113	1	HY47_MOUSE
8	320.5	52.2	116	1	HY60_MOUSE
9	318	51.8	117	1	HY26_HUMAN
10	315.5	51.4	135	1	HY02_XENLA
11	314	51.1	129	1	HY2F_HUMAN
12	311	50.7	117	1	HY62_MOUSE
13	303	49.3	119	1	HY2C_HUMAN
14	294.5	48.0	120	1	HY2B_HUMAN
15	290	47.2	136	1	HY01_XENLA
16	289.5	47.1	126	1	HY2A_HUMAN
17	284	46.3	121	1	HY2J_HUMAN
18	284	46.3	125	1	HY2D_HUMAN
19	282	45.9	121	1	HY01_MOUSE
20	279.5	45.5	122	1	HY3A_HUMAN
21	279	45.4	120	1	HY03_MOUSE
22	278	45.3	115	1	HY3D_HUMAN
23	277.5	45.2	136	1	HY2C_RABIT
24	275.5	44.9	122	1	HY3T_HUMAN
25	274.5	44.7	116	1	HY40_MOUSE
26	274.5	44.7	119	1	HY40_MOUSE
27	274.5	44.7	136	1	HY16_MOUSE
28	273	44.5	117	1	HY2B_RABIT
29	272	44.3	121	1	HY2E_HUMAN
30	270.5	44.1	139	1	HY07_MOUSE
31	269	43.8	140	1	HY02_MOUSE
32	269	43.8	142	1	HY01_RAT
33	269	43.8	147	1	HY2H_HUMAN

34	268.5	43.7	119	1	HY37_MOUSE	P01807 mus musculu
35	268	43.6	117	1	HY41_MOUSE	P01811 mus musculu
36	268	43.6	119	1	HY41_HUMAN	P01773 homo sapien
37	267.5	43.6	114	1	HY2A_RABIT	P01827 oryctolagus
38	267.5	43.6	118	1	HY51_MOUSE	P06330 mus musculu
39	267.5	43.6	119	1	HY38_MOUSE	P01808 mus musculu
40	266.5	43.4	117	1	HY3C_HUMAN	P01764 homo sapien
41	266	43.3	117	1	HY42_MOUSE	P01812 mus musculu
42	266	43.3	123	1	HY19_MOUSE	P01788 mus musculu
43	265	43.2	117	1	HY12_MOUSE	P01756 mus musculu
44	265	43.2	118	1	HY39_MOUSE	P01809 mus musculu
45	264.5	43.1	120	1	HY50_MOUSE	P06329 mus musculu

ALIGNMENTS

RESULT 1  
ID HY43\_MOUSE STANDARD; PRT; 144 AA.  
AC P01819:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region MOPC 141 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81012133; PubMed=6774258;  
RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;

"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes."  
RL Nature 286:676-683(1980).  
-I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES ICG2B.

-----  
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-----

CC EMBL: J00491; AAA8121.1; -;  
DR EMBL: V00768; CAA24149.1; -;  
DR PIR: A02094; G2MS14.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IG; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.  
FT NON\_TER 144 144  
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 59.9%; Score 368; DB 1; Length 144;  
Best local similarity 61.1%; Pred. No. 3,9e-30;  
Matches 77; Conservative 16; Mismatches 27; Indels 6; Gaps 3;

QY 1 QVQLQESGSLVSPQSLTLCTVSGFSLTKYGVSNVRQAPGKALEMLGCVSGSALTAVN 60  
DB 20 QVQLQESGSLVSPQSLTLCTVSGFSLTKYGVSNVRQAPGKALEMLGCVSGSALTAVN 79  
QY 61 TALQSRLESTRTSKSQRSLSSVTTEDTATLYYCAKSYN---GDSVPY-GLDWSPGL 115  
DB 80 STLKSRLESTRTSKSQRSLSSVTTEDTATLYYCAKSYN---GDSVPY-GLDWSPGL 138

Y	116	LTWSS	121
Db	139	SVTVSS	144
RESULT	2		
ID	HV46_MOUSE	STANDARD:	PRT: 137 AA.
AC	P018622		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Ig heavy chain V region MOPC 315 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN	NCBI_taxonomy:10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89238351; PubMed=2497341.		
RA	Ridder A., Horne C., Dorrington K.J., Klein M.;		
RT	"Cloning, sequencing and expression of the rearranged MOPC 315 VH		
RL	gene segment.";		
RL	Mol. Immunol. 26:431-434(1989).		
RN	[2]		
RP	SEQUENCE OF 1-31.		
RX	MEDLINE=78094473; PubMed=414225;		
RA	Jilka R.L., Pestka S.;		
RT	"Amino acid sequence of the precursor region of MOPC-315 mouse		
RT	immunoglobulin heavy chain.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).		
RN	[3]		
RP	SEQUENCE OF 1-21.		
RX	MEDLINE=79148738; PubMed=428562;		
RA	Schechter I., Wolf O., Zemell D., Burstein Y.;		
RT	"Structure and function of immunoglobulin genes and precursors.";		
RL	Fed. Proc. 38:1839-1845(1979).		
RN	[4]		
RP	SEQUENCE OF 19-136.		
RX	MEDLINE=7417079; PubMed=4524622;		
RA	Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;		
RT	"Amino-acid sequence of the variable region of the heavy (alpha)		
RT	chain of a mouse myeloma protein with anti-hapten activity.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).		
RN	[5]		
RP	REVISION TO 53.		
RX	MEDLINE=77244979; PubMed=268248;		
RA	Hood L., Margolies M.N., Givol D., Zakut R.;		
RT	Unpublished results, cited by:		
RL	Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;		
RL	Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).		
CC	-1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA		
CC	PROTEIN THAT HAS ANTI-DINTROPHENYL ACTIVITY.		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
CC	EMBL; M27638; AAA61337.1; -		
DR	EMBL; X07880; CAA30727.1; -		
DR	PIR; P10102; AVMS35.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IGV_1.		
KV	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	18
FT	CHAIN	19	137
FT	DOMAIN	19	48
FT			IG HEAVY CHAIN V REGION MOPC 315.
FT			FRAMEWORK-1.

```

FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFD 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G -> GG (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G -> H (IN REF. 2).
FT CONFLICT 17 78 GY -> YG (IN REF. 4).
FT CONFLICT 102 102 N -> D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; PB3828304C2B8IDC CRC64;

Query Match 57.2%; Score 351; DB 1; Length 137;
Best Local Similarity 59.0%; Pred. No. 1,9e-28;
Matches 72; Conservative 17; Mismatches 27; Indels 26; Gaps 3;

QY 2 VOLQSGPSLVKPSQTLSLCTVSGFSLT-RYGVSWRQAPKALEMIGVSSGALRAYN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 VOLQSGGVLKPSQSLSLCTSVGYSITSGYFWMWIRQPGNKLKLEMGFIKIDGSMGXN 79
    ::::: ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
QY 61 TALQSRLEVTMDTSKQSPSLSSVTTTDDTAIIYCAKAVNDSP-YGLDWSGGLLT 119
    ::::: ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
DB 80 PSLKRVASITRDTSENQFLKLSNVTEDTATYCA---GDNDHLYFDYWGQGTTLTV 135
    ::|||
QY 120 SS 121
DB 136 SS 137

RESULT 3
ID HV45_MOUSE STANDARD: PRT; 116 AA.
AC P01821:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MC101 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82075900; PubMed=6273429;
RA Katakota T., Nikaido T., Miyata T., Moriwaki K., Honjo T.;
RT "The nucleotide sequences of rearranged and germ-line immunoglobulin
RT VH genes of a mouse myeloma MC101 and evolution of VH genes in
RT mouse.";
RT J. Biol. Chem. 257:277-285(1982).
RL -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00502; AAA38515.1; -.
DR PIR; A02096; GIM510.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION MC101.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

```

```
Query Match          55.0%; Score 338; DB 1; Length 116;
Best Local Similarity 64.9%; Pred. No. 3.1e-27;
Matches 63; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

OY 1 QVQLQESGPELVPSQTLSTCTVSGFSLTKRYGVSWVROAPGKALEMLGVSAGLTAYN 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 QVQLKSGGELVNPQSLSITCTVSGFSLTKRYGVSWVROAPGKALEMLGVSAGLTAYN 79

OY 61 TALQSRSLVTRDTSKQSFSLSSVTTEDTAIYYCA 97
    ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 AAFISRLSLSKDNKSKQVFPKMNLSNDPTAIYYCAR 116

RESULT 4
HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
    of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V00767; CAA24148.1; -
DR PIR: A02095; HYMS14.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DDA4843D500 CRC64;
```

```
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR: A02101; G1H0H2.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
```

```
Query Match          54.5%; Score 334.5; DB 1; Length 146;
Best Local Similarity 52.4%; Pred. No. 9.2e-27;
Matches 66; Conservative 20; Mismatches 35; Indels 5; Gaps 1;

OY 1 QVQLQESGPELVPSQTLSTCTVSGFSLTKRYGVSWVROAPGKALEMLGVSAGLTAYN 60
    |||||:| |||||:|||||:| | | | | | | | | | | | | | | | | | | | | | |
DB 21 QVQLQMGAGLVPRSESLTCAVFGSFGYKWSATROPPRGRLERIGELNHSGRINRK 80

OY 61 TALQSRSLVTRDTSKQSFSLSSVTTEDTAIYYCAKSV-----NGDSVPYGLDYNSPGL 115
    |:|:|:|:|:|:|:|:|:| | | | | | | | | | | | | | | | | | | | | |
DB 81 TSLKSRVLTISLDPSKFNFSILKSSVTADTAIVYVCARGLLRGGMNDVYYGMDVMCGGT 140

OY 116 LITVSS 121
    :||||
DB 141 TVTVSS 146

RESULT 6
HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC 1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR: JTO508; HYMS1B.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
```

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61 TALOSRLSVTRDRSKSQFSLSSLTTEDTAIYICAKSVNGDSVPGLDIWSPGLLTYS
QY :::::|||||: | |:::|||| | |:: | | | |::|

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RP SEQUENCE.  
RX MEDLINE=77242302; PubMed=407927;

```

RN NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoyak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL 18
FT CHAIN 19 135
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 51.4%; Score 315.5; DB 1; Length 135;
Best Local Similarity 47.5%; Pred. No. 6,76-25;
Matches 56; Conservative 26; Mismatches 33; Indels 3; Gaps 1;

QY 4 LOESGPSLYKRSSQTLSTCTVSGFSLTXYGSVWRQAGCKRLKLEWLGVSGLATRYNTAL 63
Db 21 LOESGPSYGVKPESESRCTVSGFELSSYHNMWIKPQKGLGWTGATGASTAIADSL 80

QY 64 QSRSLVTRDTEKRSQFSLSSVTTEDTAIIYCAKSVNGDSVPYGLDYSPELLLTVSS 121
Db 81 KNRVITITFDNCKRKQYVLLQMGMEVYKDTAMYYCAREY---ASGYNDYWGQGTMTVTVTS 135

RESULT 11
HV2F_HUMAN
ID ID HV2F_HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debilre B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
CC PROTEIN.
CC PIR: A02099; D2HUWA.
CC HSSP: P01825; 7PAB.
CC GlycoSiteDB: P01824;
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.

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KM Immunoglobulin V region.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 51.1%; Score 314; DB 1; Length 129;  
 Best Local Similarity 49.2%; Pred. No. 9e-25;  
 Matches 65; Conservative 22; Mismatches 31; Indels 14; Gaps 3;

OY 1 QVQLQESGSLVSPQSLTCTVSGFSLT--FKYGVSWRQAPGKALEMLGVSSGALTA 58  
 Db 1 RQLQESGSLVSPQSLTCTVSGFSLTCTVSGFPIRRCIYWGMIROPKGLKLEMLGVSSGALTA 60  
 OY 59 YNTALQSLSVTRDTSKQPSLSLSSVTEDTAIYYCAKSVNGDSVPY-----GLD 109  
 Db 61 YNSLGRVYTIISVDTSRNPFSLRLMSADPAMYCAR---GNPPPYDGTGSDGID 117  
 OY 110 YMSPGLLTVSS 121  
 Db 118 VMGGFTVHVS 129

RESULT 12  
 HV62\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18533;

DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 733 precursor.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/CJ  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malpietro U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during  
 the primary immune response."  
 RT J. Exp. Med. 169:2007-2019(1989).  
 RL PIR: J0510; HVM573.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT CHAIN 1 18  
 FT SIGNAL 19 117 IG HEAVY CHAIN V REGION 733.  
 FT DISULFID 40 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 50.7%; Score 311; DB 1; Length 117;  
 Best Local Similarity 59.2%; Pred. No. 1.6e-24;  
 Matches 58; Conservative 19; Mismatches 19; Indels 2; Gaps 1;

OY 2 VOLESGLVSPQSLTCTVSGFSLT--KYGVSWRQAPGKALEMLGVSSGALTA 59  
 Db 20 VQLQESGSLVSPQSLTCTVSGFSLTCTVSGFPIRRCIYWGMIROPKGLKLEMLGVSSGALTA 79  
 OY 60 NTAQSLSVTRDTSKQPSLSLSSVTEDTAIYYCAK 97  
 Db 80 NPSPKSRITTRDTSKQPSLSLSSVTEDTAIYYCAK 117

RESULT 13  
 HV2C\_HUMAN STANDARD; PRT; 119 AA.  
 AC P01816;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region DAW.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=70258837; PubMed=5449120;  
 RA Press E.M., Hogg N.M.;  
 RT "The amino acid sequences of the Fd fragments of two human gamma-1  
 heavy chains."  
 RT Biochem. J. 117:641-660(1970).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM THE  
 SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.  
 DR PIR: A02091; G1HDM.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region.  
 FT MOD\_RES 1 1  
 FT NON\_TER 119 119 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 49.3%; Score 303; DB 1; Length 119;  
 Best Local Similarity 51.2%; Pred. No. 1e-23;  
 Matches 63; Conservative 22; Mismatches 32; Indels 6; Gaps 2;

OY 1 QVQLQESGSLVSPQSLTCTVSGFSLT--KYGVSWRQAPGKALEMLGVSSGALTA 58  
 Db 1 QVTLRESGSLVSPQSLTCTVSGFSLTCTVSGFPIRRCIYWGMIROPKGLKLEMLGVSSGALTA 60  
 OY 59 YNTALQSLSVTRDTSKQPSLSLSSVTEDTAIYYCAKSVNGDSVPYGLDYSPELLLT 118  
 Db 61 YGASLETRLAVSKDTSKQPSLSLSSVTEDTAIYYCAKSVNGDSVPYGLDYSPELLLT 116  
 OY 119 VSS 121  
 Db 117 VSS 119

RESULT 14  
 HV2B\_HUMAN STANDARD; PRT; 120 AA.  
 AC P01815;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-II region COR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=70258837; PubMed=5449120;  
 RA Press E.M., Hogg N.M.;  
 RT "The amino acid sequences of the Fd fragments of two human gamma-1  
 heavy chains."  
 RT Biochem. J. 117:641-660(1970).  
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA  
 PROTEIN.  
 DR PIR: A02089; G1HUCO.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 FT MOD\_RES 1 1  
 FT DISULFID 22 94 PYRROLIDONE CARBOXYLIC ACID.



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099NG4
ID 099NG4 PRELIMINARY: PRT: 121 AA.
AC 099NG4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Mus musculus (Mouse).
OG Plasmid pHEB1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RA Bausch W., Kola A., Klos A., Koehl J.;
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL: AJ222590; CAA10890.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003599; Iq.
DR InterPro: IPR003600; Iq_Like.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_v.
DR Pfam: PF00047; Iq_1.
DR SMART: SM00409; Iq_1.
DR SMART: SM00406; Iq_v_1.
DR SMART: SM00410; Iq_Like; 1.
KM Plasmid.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EB8C95D5B CRC64;

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Query Match          59.7%; Score 366.5; DB 11; Length 121;
Best Local Similarity 60.0%; Pred. No. 2.7e-30;
Matches 75; Conservative 14; Mismatches 27; Indels 9; Gaps 2;

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QY 1 QVQLQESGSPSLVPSQSLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 QVQLKESGPGLVAPSGSLSTCTVSGFPLTSHGVSWVRQPGKLEMLGIVMGDKMTKYH 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKSQFSLSSTVTEPTAIYYCA----KSYNGDSVPGGLDYSPGLL 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 SALISRLSISKDNSKQVFLKLSLTQEDTATFYCARHYKYKAN-----YAMDYMGQGS 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 117 LTVSS 121
    |||||
DB 116 LTVSS 120

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RESULT 3
Q96EYO PRELIMINARY: PRT: 613 AA.
AC 096EYO;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILLS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011857; AAH11857.1; -.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

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Query Match          58.9%; Score 361.5; DB 4; Length 613;
Best Local Similarity 58.7%; Pred. No. 6.9e-29;
Matches 74; Conservative 17; Mismatches 24; Indels 11; Gaps 2;

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QY 1 QVQLQESGSPSLVPSQSLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 QVQLQESGPGLVAPSGSLSTCTVSGSISYWSVRQPGKLEMLGIVMGDKMTKYH 79
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKSQFSLSSTVTEPTAIYYCAKSYNGDSVPGGLDYSPGLL 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 PSLKSRVTMSVDTSKNQFSLKLSLTAAADTAYYYCA-----SQRELPTVGLFTWGQGT 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 LTVSS 121
    |||||
DB 134 LTVSS 139

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RESULT 4
Q9UL73 PRELIMINARY: PRT: 119 AA.
AC 09UL73;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035041; AAD56277.1; -.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_v.
DR Pfam: PF00047; Iq_1.
DR SMART: SM00406; Iq_v_1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

```

```

Query Match          58.3%; Score 358; DB 4; Length 119;
Best Local Similarity 57.9%; Pred. No. 2e-29;
Matches 70; Conservative 18; Mismatches 31; Indels 2; Gaps 1;

```

```

QY 1 QVQLQESGSPSLVPSQSLTCTVSGFSLTKYGVSWVRQAPGKALEMVGSSGALTAYN 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 QVQLQESGPGLVAPSGSLSTCTVSGSISYWSVRQPGKLEMLGIVMGDKMTKYH 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TALQSLRYTRPTSKSQFSLSSTVTEPTAIYYCAKSYNGDSVPGGLDYSPGLLTVS 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 PSLKSRVTMSVDTSKNQFSLKLSLTAAADTAYFYCARLSNMG--PYFDYMGQGTLYVS 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 S 121
    |
DB 119 S 119

```

```

RESULT 5
Q95973 PRELIMINARY: PRT: 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)

```

Query Match	54.58;	Score	334.5;	DB	4;	Length	150;
Best Local	Similarly	54.58;	Pred. No.	7e-27;			
Matches	67;	Conservative	20;	Mismatches	29;	Indels	7;
						Gaps	2;

OY		1	OVQLQESPSLVKPKSQTLSLCTVSGFSL--TKYGVSVMRQAAPGALAEWLGGSSGALT	58
Dy			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Dd		20	OLQLQESPGVLKKPSETILSLSTCVSGGSISNMYWGVTROPPEKGLEIGSSLHNSGDY	79
OY		59	YNIAQSGLSTRDTSKSQSFSLSSSYTTEDTAITYCAKSVDGVPPGLDYSPCLILT	118
Dy			:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Dd		80	YNPSLKSHSVTTISVDTSKNQFSLRLSSYYTAADPAAYVCARLGMG-----AFDEWGHGTWT	134
OY		119	VSS 121 	
Dd		135	VSS 137	
RESULT		6		
O9BQB8	ID	O9BOB8	PRELIMINARY;	PRT;   597 AA.
AC	O9BOB8:			
DT	01-JUN-2001	(TREMBLrel. 17,	Created)	
DT	01-JUN-2001	(TREMBLrel. 17,	Last sequence update)	
DT	01-Dec-2001	(TREMBLrel. 19,	Last annotation update)	
De	UNKNOWN	(PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).		
OS	Homo sapiens	(Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=RHABDOMYOSARCOMA;			
RA	Strausberg R.;			
RL	Submitted (Apr-2001) to the EMBL/GenBank/DDBJ databases. [2]			
RN	RP	SEQUENCE FROM N.A.		
RC	TISSUE-Lymphoma;			
RA	Strausberg R.;			
DL	EMBL; BC006180; AHH06180.1;			
DR	EMBL; BC001872; AAAH01872.1;	-		
DR	HSSP; P01825; FFAE.			
DR	InterPro; IPR003599; Ig_			
DR	InterPro; IPR003597; Ig_cl.			
DR	InterPro; IPR003600; Ig_like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			

Query Match	54.28;	Score 333;	DB 4;	Length 597;
Best Local Similarity	52.08;	Pred. No. 5.8e-26;		
Matches 65;	Conservative 20;	Mismatches 36;	Indels 4;	Gaps 1;

```

OY 1 OV0LDESGBSLVKKPSOTLSLTCTVSGFSLTKYGVSWVR0APKALEMLGVSAGALTAYN 60
    | | | | : | : | | | | | | | | : | : | | | | | | : : : | |
Db 20 OV0LODMWAGLKKPSETTSLTCTGVVGGSGFYWSHROPPKGLGEMJELHNSGITN 79
    | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 TALOSRLSVTRDTSKQSFSLSSVTTEDTAIYCAKSYN---GDSVPYGLDYSPGILL 116
    | : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 80 PELKSRVITSVDTSKQSLKSLSSVNADTAIYVCARVITRASPGIDGRYGMVDVGGCTT 139
    | : | | | : | | | | | | | | | | | | | | | | | | | | | |
OY 117 LTVSS 121
    : | | | |
Db 140 VTVSS 144

```

RESULT	7
Q99M22	
ID	Q99M22
PRELIMINARY;	
PRT;	479 AA.

```

AC Q09M22:2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEITICAL 52.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;
RA Strausberg R.;
RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AAH02091.1; -.
DR HSSP; P01810; 2FRJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_1like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

```

Query Match	53.7%	Score 330	DB 11	Length 479
Best Local Similarity	54.0%	Pred. No. 9e-26		
Matches 67, Conservative	20	Mismatches 12	Gaps 3	

[illegible]

QY 118 TVSS 121  
111:  
DB 132 TVSA 135

## RESULT 8

Q9UL96 PRELIMINARY; PRT; 121 AA.

AC Q9UL96; PRELIMINARY; PRT; 121 AA.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".  
RU Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035018; AAD56254.1; -.  
DR HSSP: P01825; 7FAB.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 121;  
Best Local Similarity 54.5%; Pred. No. 2e-26;  
Matches 67; Conservative 20; Mismatches 32; Indels 4; Gaps 2;

QY 1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 58  
1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 58  
DB 1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 60  
QY 59 YNTALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVNDSPYGLDYSFGILLT 118  
1 YNTALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVNDSPYGLDYSFGILLT 118  
DB 61 YNTALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVNDSPYGLDYSFGILLT 118  
QY 119 VSS 121  
111  
DB 119 VSS 121

## RESULT 9

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10; PRELIMINARY; PRT; 597 AA.  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 65.3 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph, LYMPHOMA;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC002963; AAH02963.1; -.  
HSSP: P01825; 7FAB.

DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003597; Ig\_c1.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 5.  
DR SMART: SM00409; IGV; 2.  
DR SMART: SM00407; IGV; 4.  
DR SMART: SM00406; IGV; 1.  
DR SMART: SM00410; IGV-like; 1.  
DR PROSITE: PS00290; Ig\_MHC; UNKNOWN\_3.  
KW Hypothetical protein.  
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8FB7E055851 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 597;  
Best Local Similarity 52.0%; Pred. No. 1.5e-25;  
Matches 65; Conservative 19; Mismatches 37; Indels 4; Gaps 1;

QY 1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 60  
1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 60  
DB 20 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 79  
QY 61 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 116  
1 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 116  
DB 80 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 139  
QY 117 TVSS 121  
111  
DB 140 TVSS 144

## RESULT 10

Q96AA6 PRELIMINARY; PRT; 618 AA.

AC Q96AA6; PRELIMINARY; PRT; 618 AA.  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 67.8 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph, AND LYMPHOMA;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC017356; AAH17356.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 618 AA; 67758 MW; 96BBD4C7C696E0A6 CRC64;

Query Match 53.6%; Score 329; DB 4; Length 618;  
Best Local Similarity 52.0%; Pred. No. 1.6e-25;  
Matches 65; Conservative 19; Mismatches 37; Indels 4; Gaps 1;

QY 1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 60  
1 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 60  
DB 20 QVLOQESGPLVKSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVSAGALTA 79  
QY 61 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 116  
1 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 116  
DB 80 TALQSRSLVTRDTSKQSFSLSSVTTEDETAIYYCAKSVN----GDSVPYGLDYSFGILL 139  
QY 117 TVSS 121  
111  
DB 140 TVSS 144

## RESULT 11

Q96KX8

ID Q96KX8 PRELIMINARY: PRT: 496 AA.  
AC Q96KX8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHEICAL 53.4 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC016369; AAH16369.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 496 AA: 53391 MW: D346929849040D69 CRC64;

Query Match 52.7%; Score 323.5; DB 4; Length 496;  
Best Local Similarity 53.2%; Pred. No. 4.4e-25;  
Matches 66; Conservative 20; Mismatches 35; Indels 3; Gaps 2;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSL--TKYGVSWVRQAPGKALEWLGSSGALTA 58  
DB 20 QVQLQESGPGLVKSEETISLTCTVSGSISSSYYMGWIRQPGKLEMIATYYSGITY 79  
QY 59 YNTALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVGDSVPYG-LDYSPGLLL 117  
DB 80 YNPSTKSRVITISVDTSKQSLKRVSYAADPAVYCAHGRSGRGIGALIDYWGCGTLY 139  
QY 118 TVSS 121  
DB 140 TVSS 143

RESULT 12  
Q9UL75 PRELIMINARY: PRT: 122 AA.  
AC Q9UL75;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; Pubmed-9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RT Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035039; AAD56275.1; -.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA: 13719 MW: 56CDB0612586A6529 CRC64;

Query Match 51.7%; Score 317.5; DB 4; Length 122;  
Best Local Similarity 52.0%; Pred. No. 3.1e-25;  
Matches 66; Conservative 20; Mismatches 30; Indels 11; Gaps 4;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSLTKYGV---SWVRQAPGKALEWLGVS--SSGAL 56  
DB 1 QVQLQESGPGLVKPSQTLSTCTVCAISGDSVSNNAAMNWRQSPRLKLEWLGRIYYSKRY 60  
QY 57 YNTALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVN--GDSVPYGLDYSPG 114  
DB 61 NDYRVSKSRITINPDTSKNQSFSLQINSVYTPEDTAVYCAKDLELIGQ-----FDWCGG 115  
QY 115 LLTVSS 121  
DB 116 LLTVSS 122

RESULT 13  
Q9Y509 PRELIMINARY: PRT: 147 AA.  
AC Q9Y509;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE VH3 PROTEIN (FRAGMENT).  
CN VH3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96071149; Pubmed-7475288;  
RA Cao J., Vesic R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,  
RA Lichtenstein A.K., Berenson J.R.;  
RT "A CD10-positive subset of malignant cells is identified in multiple  
RT myeloma using PCR with patient-specific immunoglobulin gene primers";  
RL Leukemia 9:1948-1953(1995).  
DR EMBL; S80860; AAD14359.1; -.  
DR HSSP; P01772; 2E84.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
SQ SEQUENCE 147 AA: 15768 MW: 8489FCAA7BC925C CRC64;

Query Match 49.8%; Score 305.5; DB 4; Length 147;  
Best Local Similarity 48.4%; Pred. No. 6.7e-24;  
Matches 61; Conservative 25; Mismatches 35; Indels 5; Gaps 3;

QY 1 QVQLQESGPSTLVKPSQTLSTCTVSGFSLTKYGVSWVRQAPGKALEWLGVS--SGALTA 59  
DB 1 QVHLVSGGGVYQPKSLRLSCASGFTSTYGMWVRQAPGKGLDWMALISVDSSTGY 60  
QY 60 YNTALQSLRSLVTRDTSKQSFSLSSVTTEDTAIYCAKSVN--GDSVPY---GLDYSPGL 115  
DB 61 AGSVKGRFTISRDNSKNTLYQMTSLRVEDTAIVYCAKKGNYFDSVGYAGIDYWGQGT 120  
QY 116 LLTVSS 121  
DB 121 LLTVSS 126

RESULT 14  
Q96BB9 PRELIMINARY: PRT: 597 AA.  
AC Q96BB9;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHEICAL 65.0 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;



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OM of: US-09-786-015-4 to: GenEmbl:\* out\_format : pfs  
Date: Aug 12, 2002 10:39 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

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-O=MODEL-frame+p2n.model -DEV=xlp  
-O/cgn2.1/USPTO_spool/US09786015/runat_1082002.092422.53/app-query.fasta.1.347  
-DB=genembl -QEMT=fastcap -SUFFIX=p2n.rge -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -VGAPOP=10.000 -VGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NOR-ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09786015@cgn1.1.7012 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
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## Search information block:

Query: US-09-786-015-4  
Query length: 111  
Database: GenEmbl:\*  
Database sequences: 1797656  
Search length: 1873333701  
Search time (sec): 1937.690000

## score\_list:

Sequence	Strd Orig	EScore	EScore Len	Documentation
gb.com:BTU32261	+	455.00	818.22	3.2e-37
gb.com:AF172696	+	451.50	813.46	5.9e-37
gb.com:AF172691	+	447.00	805.26	1.7e-36
gb.com:AF172690	+	446.00	803.46	2.1e-36
gb.com:AF172689	+	445.00	801.66	2.7e-36
gb.com:AF015795	+	444.50	800.75	3.0e-36
gb.com:AF015792	+	443.50	798.94	3.8e-36
gb.com:AF172684	+	442.00	796.42	5.4e-36
gb.com:AF172686	+	441.50	795.42	6.0e-36
gb.com:AF172687	+	441.50	795.42	6.0e-36
gb.com:AF015798	+	440.50	793.53	7.7e-36
gb.com:AF015799	+	440.50	793.53	7.7e-36
gb.com:AF015801	+	440.50	793.53	7.7e-36
gb.com:AF172688	+	439.50	791.64	9.7e-36
gb.com:AF172683	+	439.00	790.82	1.1e-35
gb.com:BTU32250	+	439.00	789.21	1.3e-35
gb.com:AF172700	+	438.50	790.17	1.2e-35
gb.com:AF015797	+	435.00	783.69	2.7e-35
gb.com:AF172697	+	433.00	779.99	4.3e-35
gb.com:AF109697	+	430.00	774.66	8.6e-35
gb.com:BTU31106	+	430.00	773.10	1.1e-34
gb.com:BTU32253	+	430.00	773.10	1.1e-34
gb.com:AF015791	+	429.50	773.68	9.8e-35
gb.com:AF015793	+	429.50	773.68	9.8e-35
gb.com:AF172698	+	429.50	773.60	9.9e-35
gb.com:AF023841	+	429.00	772.70	1.1e-34
gb.com:BTU32234	+	429.00	771.39	1.3e-34
gb.com:AF172699	+	428.50	771.79	1.2e-34
gb.com:AF015796	+	428.00	771.05	1.4e-34
gb.com:AF023843	+	427.00	769.25	1.7e-34
gb.com:BTU32249	+	425.00	764.08	3.3e-34
gb.com:BTU32695	+	424.00	763.75	3.5e-34
gb.com:AF172692	+	422.50	761.13	4.5e-34
gb.com:BTU32602	+	422.50	759.24	5.0e-34
gb.com:AF015800	+	421.50	757.97	6.2e-34
gb.com:AF015809	+	420.00	756.64	7.0e-34
gb.com:AF040919	+	418.00	748.67	2.4e-33
gb.com:AF172682	+	417.00	751.12	1.8e-33
gb.com:AF015809	+	416.00	749.40	2.2e-33
gb.com:AF172701	+	416.00	749.32	2.2e-33

gb.com:BTU012803 + 415.50 748.33 2.5e-33 336 | AU012803 Bos taurus mRNA for  
gb.com:BTU11633 + 414.00 744.72 4.0e-33 332 | U11633 Bos taurus B11 cell-1  
gb.com:AF172694 + 413.00 743.74 4.5e-33 339 | AF172694 Ovis aries clone 47  
gb.com:BTU012804 + 412.50 742.76 5.1e-33 342 | AU012804 Bos taurus mRNA for  
gb.com:AF040904 + 409.50 731.94 2.1e-32 626 | AF040904 Ovis aries Immunogl

seq\_name: gb.com:BTU32261

seq\_documentation\_block:

LOCUS BTU32261 393 bp mRNA linear MAM 25-APR-1996  
DEFINITION Bos taurus clone 16 Immunoglobulin lambda light chain variable  
region (Vlambda) mRNA, partial cds.

ACCESSION U32261

KEYWORDS U32261.1 GI:1276622

SOURCE cow.

ORGANISM Bos taurus

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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JOURNAL

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AUTHORS

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JOURNAL

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misc_feature	220..240 /gene="V1ambda1a" /note="encodes complementarity-determining region 2 "
misc_feature	241..336 /gene="V1ambda1a" /note="encodes framework region 3 "
misc_feature	337..366 /gene="V1ambda1a" /note="encodes complementarity-determining region 3 "
misc_feature	367..393 /gene="V1ambda1a" /note="encodes framework region 4 "
BASE COUNT	74 a 132 c 105 g 82 t
ORIGIN	

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  Ratio: 4.461         Gaps: 0
Percent Similarity: 93.578  Percent Identity: 81.651
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alignment\_block:  
US-09-786-015-4 x BTU32261

Align seg 1/1 to: BTU32261 from: 1 to: 393

1 GlnAspValLeuThrhGlnProSerSerValSergIySerLeuGlyInar 17  
11 |  
67 CAGCGTGTCTACTACACGCCGTCCTCCGTGC GGATCCTCGGGCCAGAG 116  
17 gvalSerIleThrCySerSergIySerSerAsnIleGlyGlysnalAr 34  
117 GGHCTCATCACCTGCTCTGGAGAGCAGCAGCAAGTTGGAACTGGCAATT 166  
34 yYValGlyTrpPyArgInGlnValProGIYSerAlaProArgLeuLeuIle 50  
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::  
167 ATGTGAGCGTGTTTCCACAGATCCCGAGGATGGGCCCCAGAACCTCATC 216  
51 SerAlaThrThrAspArgAlaSergIyIleProAspArgPheSerGlyse 67  
217 TATGGGCGACCAAGTCGAGACCCTGGGGGTGCCCCACGCAATTCTCGGCTC 266  
67 rArgSerGIyAsnThrAlaThrLeuThrIleSerSerLeuGlnIlaIua 84  
267 CAGGTGTGGGAACACAGCCACCCTGACATCATAGCTCGCTCAGGCTAGG 316  
84 spcIuaIlaaspyrTyrcysAlaSerTyrgInSerThrTyrsGlyVal 100  
317 ACAGAGCAGAATTAATTCTGTGCATCTTATCAGAGTAGTAACACAGCTGTG 366  
101 PheGlySerGlyTythrArgLeuThrVal 109  
67 TTGGCGCAGGGGAGCACCACTGACGCTC 393

seq\_name: gb\_om:AF172696

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seq_documentation_block:
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LOCUS	AE172696	330 bp	mRNA	linear	MAM 29-AUG-1999
DEFINITION	Ovis aries clone 53 immunoglobulin light chain variable region				

(IGLV) mRNA, partial cds.

VERSION AF172696.1 GI:5802439

## KEYWORDS

**SOURCE** sheep.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Bovidae; Caprinae; Ovis.  
1 (bases 1 to 330)  
White,G.P., Meusen,E.N.T. and Newton,S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
nematode parasite *Haemonchus contortus*  
unpublished  
2 (bases 1 to 330)  
White,G.P., Meusen,E.N.T. and Newton,S.E.  
Direct Submission  
Submitted (26-JUL-1999) School of Veterinary Science, The Centre

**AUTHORS** White, G.P., Meusen, E.N.T. and Newton, S.E.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (26-JUL-1999) School of Veterinary

for Animal Biotechnology, The University of Melbourne, Parkville  
Melbourne, Victoria 3052, Australia

FEATURES	Location/Qualifiers
source	1. .330

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1 330

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CDS

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/product="immunoglobulin light chain variable region"
/protein_id="AA051686.1"
/db_xref="GI:580240"
/translation="QAVLTQSSSESGIQAVSTTCSSSSNIGRGYNKYQVPGSG
PKLLIVATTIRASGVPPRFSGSRSGNATATITISLQAEADYCAYSKNSYGIFGS
GTRLTIVG"

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BASE COUNT	66 a	101 c	90 g	73 t
ORIGIN				

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  Percent Similarity: 91.892
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  Gaps: 1
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alignment_block:
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Align seg 1/1 to: AF172696 from: 1 to: 330

[illegible]

67 rArgSerGlyAsnThrAla

198 CAGATCTGGCAACACAGC

84 spglaiaasptyrtyrcysalaserTyrGlnserThrTyrserGlyval 1000

1  
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101 pheglyserglyThrargLeuthrValleugly 111

298 TTCGGCAGCGGGACCAAGCTGACCGTCTGGGT 330

seq\_name: gb\_om:AF172691



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|||||
51 TGTCTCCATCACTGCTCTGGAGCAGTACGCTGATATGTAATT 100
34 YVVALGTYTPYRGLNGINValProGlySerAlaProArgLeuLeu 50
101 ATGTAGAGTGTGTCACATCACTCCAGATCAGCCCAAACTCTCAT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
151 TATGTGTCAGCCAGTCGAGCCTCGGGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
201 CAGGCTGTCACACAGCAGCTGACATCAGCTCGCTCCAGGCTGAGG 250
84 SPGLALASPtyrTyrcysAlaSerTyrglnSerThrTyrsSerGlyAl 100
251 ACGAGCGCATTTACTGTGCTGATTTATGACAGCAGTACGAGTGTGCT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
301 TTCGGCAGCGGGACCGAGCTGACGCTCGTGGGT 333

seq_name: gb_om:AF172689
seq_documentation_block:
LOCUS AF172689 333 bp mRNA linear MAR 29-AUG-1999
DEFINITION Ovis aries clone 34 Immunoglobulin light chain variable region
(GLV) mRNA, partial cds.
ACCESSION AF172689
VERSION AF172689.1 GI:5802425
KEYWORDS
SOURCE
ORGANISM
.
Sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 333)
White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
Unpublished
2 (bases 1 to 333)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
Source
1..333
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="34"
/tissue_type="abomasal lymph node"
1..333
/gene="IGLV"
<1..>333
/gene="IGLV"
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAB51679.1"
/db_xref="GI:5802426"
/translaton="QAVLTQPPSSVSRSLGQSVITSGSSSNIGYVSWYQOVPFG
APRILYGATSRASGIPDRFSGSRFGNTATLTITSLQAGDESDYCASQYTDSEIFG
SGRLTVLG"
BASE COUNT 68 a 97 c 91 g 77 t
ORIGIN
alignment_scores:
Quality: 445.00 Length: 111
Ratio: 4.450 Gaps: 0

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Percent Similarity: 90.090 Percent Identity: 81.081
alignment_block:
US-09-786-015-4 x AF172689
Align seg 1/1 to: AF172689 from: 1 to: 333
1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlnArg 17
111 |||||
1 CAGGCTGTGTCAGTACACCGCTCCGCTGTGTCAGATTCCTCGGGCAGAG 50
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyAlaAla 34
51 TGTTCATCACTGCTCTGGAGCAGCAGCAGCAGCATTTGATATGTAATT 100
34 YVVALGTYTPYRGLNGINValProGlySerAlaProArgLeuLeu 50
101 ATGTAGAGTGTGTCACATCACTCCAGATCAGCCCAAAATCTCTCAT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
151 TATGTGTCAGCCAGTCGAGCCTCGGGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
201 CAGGTTTGACACACAGCAGCTTGACATCAGCTCGCTCCAGGCTGAGG 250
84 SPGLALASPtyrTyrcysAlaSerTyrglnSerThrTyrsSerGlyAl 100
251 ACGAGCTGTCATTTACTGTGCTGATTTATGACAGCAGTACGAGTGTGCT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
301 TTCGGCAGCGGGACCGAGCTGACGCTCGTGGGT 333

seq_name: gb_om:AF015795
seq_documentation_block:
LOCUS AF015795 333 bp mRNA linear MAR 10-MAR-2000
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial
cds.
ACCESSION AF015795
VERSION AF015795.1 GI:2323379
KEYWORDS
SOURCE
ORGANISM
.
cow.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 333)
Salni,S.S., Allore,B., Jacobs,R.M. and Kaushtk,A.
Exceptionally long CDR3H region with multiple cysteine residues in
functional bovine IgM antibodies
Eur. J. Immunol. 29 (8), 2420-2426 (1999)
99387993
JOURNAL MEDLINE 10458755
REFERENCE
2 (bases 1 to 333)
Salni,S.S., Jacobs,R. and Kaushtk,A.
Direct Submission
Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada
FEATURES
Source
1..333
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BLV48"
/note="bovine x mouse heterohybridoma secreting IgM
antibody"
<1..>333
/codon_start=1
/product="immunoglobulin light chain variable region"
/protein_id="AAB6566.1"
/db_xref="GI:2323380"
CDS

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/translation="QAVLTQPSVSGSLGQRVSYITCGSSSNVNGRNVNMFQIIPGS  
APRTLYGATSRASGVDPDRFSGSRSGNTATLTITSSIQADEADYFCAAYDSSTNAVF  
GSGTTLTVL"  
BASE COUNT 65 a 106 c 94 g 68 t  
ORIGIN

alignment\_scores:  
Quality: 444.50 Length: 111  
Ratio: 4.316 Gaps: 1  
Percent Similarity: 92.793 Percent Identity: 80.180

alignment\_block:  
US-09-786-015-4 x AF015795 ..

Align seg 1/1 to: AF015795 from: 1 to: 333

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1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 CAGGCTGCTGCTGACTCAGCCGCTCCTCCGTCGCGGTCCCTCGGCGCAGAG 50
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
51 GGTCTCCATCAGCTGCTGGAAGCACAGCACAGCAAGCTTGGCGCTGCCAATT 100
34 yValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuLeuIle 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
101 ATGTGAACGTGGTTCACACAGATCCAGAGATCGGCCCCAGAACCTCATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
151 TATGTCGACAGCTGAGCCCTCTGGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGua 84
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 CAGGCTGGAACACAGCACAGCGTGCACCATCAGCTCCAGGCGCAGG 250
84 spGluAlaAspTyTyrCysAlaSerTyr...GlnSerThyTyrSerGly 99
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
251 ACGAGGCGGATTATTCTGTGCACACTTATGACAGCACTAACAAATATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 110
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 GTTTTCGGCAGCGGACACACATGACCTGACCTGCTC 333
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seq\_name: gb\_om:AF015792

seq\_documentation\_block:

LOCUS AF015792 333 bp mRNA linear MAR 10-MAR-2000  
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial  
cds

ACCESSION AF015792  
VERSION AF015792.1 GI:2323373  
KEYWORDS  
SOURCE

ORGANISM

Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 333)  
REFERENCE  
AUTHORS Salai,S., Allore,B., Jacobs,R.M. and Kaushik,A.  
TITLE Exceptionally long CDR3H region with multiple cysteine residues in  
functional bovine IgM antihodles  
JOURNAL Eur. J. Immunol. 29 (8), 2420-2426 (1999)  
MEDLINE 99387993  
PUBMED 10458755

REFERENCE  
AUTHORS Salai,S., Jacobs,R. and Kaushik,A.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,  
ON N1G 2W1, Canada

FEATURES  
source 1..333 Location/Qualifiers

/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone="BLYIG9"  
/note="bovine x mouse heterohybridoma secreting IgM  
antibody"  
CDS  
<1..>333  
/codon\_start=1  
/product="immunoglobulin light chain variable region"  
/protein\_id="AAH6563.1"  
/db\_xref="GI:2323374"  
/translation="QAVLTQPSVSGSLGQRVSYITCGSSSNVNGRNVNMFQIIPGS  
APRTLYGATSRASGVDPDRFSGSRSGNTATLTITSSIQADEADYFCAAYDSSTNAVF  
GSGTTLTVL"

BASE COUNT 66 a 103 c 94 g 70 t  
ORIGIN

alignment\_scores:  
Quality: 443.50 Length: 111  
Ratio: 4.306 Gaps: 1  
Percent Similarity: 92.793 Percent Identity: 79.279

alignment\_block:  
US-09-786-015-4 x AF015792 ..

Align seg 1/1 to: AF015792 from: 1 to: 333

```
1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 CAGGCTGCTGCTGACTCAGCCCTCCTCCGTCGCGGTCCCTCGGCGCAGAG 50
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
51 GGTCTCCATCAGCTGCTGGAAGCACAGCACAGCAAGCTTGGCGCTGCCAATT 100
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
151 TATGTCGACAGCTGAGCCCTCTGGGGTCCCGACGATTCCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGua 84
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 CAGGCTGGAACACAGCACAGCATGACCATCAGCTCCAGGCGCAGG 250
84 spGluAlaAspTyTyrCysAlaSerTyr...GlnSerThyTyrSerGly 99
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
251 ACGAGGCGGATTATTCTGTGCACACTTATGACAGCACTAATATATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 110
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
301 GTTTTCGGCAGCGGACACACATGACCTGACCTGCTC 333
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seq\_name: gb\_om:AF172684

seq\_documentation\_block:

LOCUS AF172684 333 bp mRNA linear MAR 29-AUG-1999  
DEFINITION Ovis aries clone 17 immunoglobulin light chain variable region  
(IGLV) mRNA, partial cds.

ACCESSION AF172684  
VERSION AF172684.1 GI:5802415  
KEYWORDS  
SOURCE

ORGANISM

Ovis aries  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Caprinae; Ovis.

REFERENCE  
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.  
TITLE A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal

JOURNAL nematode parasite Haemonchus contortus  
 REFERENCE Unpublished  
 AUTHORS 2 (bases 1 to 333)  
 TITLE White,G.P., Meusen,E.N.T. and Newton,S.E.  
 JOURNAL Direct Submission  
 Submitted (26-JUL-1999) School of Veterinary Science, The Centre  
 for Animal Biotechnology, The University of Melbourne, Parkville,  
 Melbourne, Victoria 3052, Australia  
 FEATURES Location/Qualifiers  
 source 1..333  
 /organism="Ovis aries"  
 /db\_xref="taxon:9940"  
 /clone="17"  
 /tissue\_type="abomasal lymph node"  
 1..333  
 /gene="IGLV"  
 <1..>333  
 /gene="IGLV"  
 /codon\_start=1  
 /product="immunoglobulin light chain variable region"  
 /protein\_id="AAD51674.1"  
 /db\_xref="GI:5802416"  
 /translation="QAVLTQPSVSRLGOSVSYTCGSSSNVGYGNVSWTQOYVGS  
 APLKIYGATSRASGVPRFSRSGRNTATLTIGSLQADEADYICAFDSSNVGVFG  
 SGRRLVYLG"

BASE COUNT 66 a 95 c 92 g 80 t  
 ORIGIN

alignment\_scores:  
 Quality: 442.00 Length: 111  
 Ratio: 4.420 Gaps: 0  
 Percent Similarity: 90.090 Percent Identity: 80.180

alignment\_block:  
 US-09-786-015-4 x AF172684 ..

Align seg 1/1 to: AF172684 from: 1 to: 333

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1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 CAGGCTGTGCTGACTCAGCGCTCCTCCGTGTCAGAGTCCCGGGCCAGAG 50
17 gValSerLeuThrGlySerGlySerSerSerAsnLeuGlyAsnAlaT 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 TGTCTCCATCACCTGCTTGGAGACAGCAGCAGCTGTGATATGTAATT 100
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ATGTGAGCTGTATCCACACAGTCCAGAGATCAGCCCCCAAACTCCTCAT 150
51 SerAlaThrThrAspArgAlaSerGlyTyrLeuProAspArgPheSerGly 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TATGAGTGCACAGCAGCGAGCTCAGGGGTCCCGCAGCATTTTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGTTCGCAACACAGCGGCTTGCACCATCAGCTCGCTCCAGGCTGAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAla 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACGAGGCCGATTATTAATGCTGATTTATGACAGCATTAATTATGCTGTT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTTCGGCAGCGGACAGCAGCTGACCTCCTGGGT 333
seq_name: gb_com:AF172686
seq_documentation_block: 330 bp mRNA linear MAM 29-AUG-1999
LOCUS AF172686
DEFINITION Ovis aries clone 14 immunoglobulin light chain variable region
(IGLV) mRNA, partial cds.
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ACCESSION AF172686  
 VERSION AF172686.1  
 KEYWORDS GI:5802419  
 SOURCE  
 ORGANISM  
 Ovis aries  
 sheep.  
 Bovidae; Caprinae; Ovis.  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 330)  
 White,G.P., Meusen,E.N.T. and Newton,S.E.  
 A single-chain variable region immunoglobulin library from the  
 abomasal lymph node of sheep infected with the gastrointestinal  
 nematode parasite Haemonchus contortus  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 330)  
 AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Centre  
 for Animal Biotechnology, The University of Melbourne, Parkville,  
 Melbourne, Victoria 3052, Australia  
 FEATURES Location/Qualifiers  
 source 1..330  
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 /db\_xref="taxon:9940"  
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 /tissue\_type="abomasal lymph node"  
 1..330  
 /gene="IGLV"  
 <1..>330  
 /gene="IGLV"  
 /codon\_start=1  
 /product="immunoglobulin light chain variable region"  
 /protein\_id="AAD51676.1"  
 /db\_xref="GI:5802420"  
 /translation="QAVLTQPSVSRLGOSVSYTCGSSSNVGYGNVSWTQOYVGS  
 APLKIYGATSRASGVPRFSRSGRNTATLTIGSLQADEADYICSSDSSFPVFG  
 GTRLVYLG"

BASE COUNT 65 a 98 c 90 g 77 t  
 ORIGIN

alignment\_scores:  
 Quality: 441.50 Length: 111  
 Ratio: 4.328 Gaps: 1  
 Percent Similarity: 91.892 Percent Identity: 81.081

alignment\_block:  
 US-09-786-015-4 x AF172686 ..

Align seg 1/1 to: AF172686 from: 1 to: 330

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1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 CAGGCTGTGCTGACTCAGCGCTCCTCCGTGTCAGAGTCCCGGGCCAGAG 50
17 gValSerLeuThrGlySerGlySerSerSerAsnLeuGlyAsnAlaT 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 TGTCTCCATCACCTGCTTGGAGACAGCAGCAGCTGTGATATGTAATT 100
34 yrValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ATGTGAGCTGTATCCACACAGTCCAGAGATCAGCCCCCAAACTCCTCAT 150
51 SerAlaThrThrAspArgAlaSerGlyTyrLeuProAspArgPheSerGly 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TTTGAGCAACAAGTCGAGCTCGGGGTCCCGCAGCATTTTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGGTTCGCAACACAGCGACTTGCACCATCAGCTCGCTCCAGGCTGAGG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAla 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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251 ACGAGCCGATTATTACTGTTCACTTATGACAGCACT...AGCTTTGTA 297
101 PheGlySerGlyThrArgLeuThrValIleuGly 111
|||||
298 TTCGGCAGCGGACCGAGCTGACCTGCTGGGT 330

seq_name: gb_om:AF172687

seq_documentation_block:
LOCUS AF172687 330 bp mRNA linear MAM 29-AUG-1999
DEFINITION Ovis aries clone 146 immunoglobulin light chain variable region
(GLV) mRNA, partial cds.
ACCESSION AF172687
VERSION AF172687.1 GI:5802421
KEYWORDS
SOURCE
ORGANISM sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 330)
White, G.P., Meusen, E.N.T. and Newton, S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 330)
White, G.P., Meusen, E.N.T. and Newton, S.E.
Direct Submission
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
source
1..330
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="146"
/tissue_type="abomasal lymph node"
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/gene="IGLV"
<1..>330
/gene="IGLV"
/codon_start=1
/product="immunoglobulin light chain variable region"
/db_xref="GI:5802422"
/translation="QAVLRQPSVSRSIGQSVSYTCSSSSNVGNGNYSWYQQYPGS
APKLIFATSRASGVPDRFSGSRSGNTATLTISLQADEADYCCSYDSSSFVFGS
GRLTVTL"
BASE COUNT 65 a 101 c 90 g 74 t
ORIGIN

alignment_scores:
Quality: 441.50 Length: 111
Ratio: 4.328 Gaps: 1
Percent Similarity: 91.892 Percent Identity: 81.081

alignment_block:
US-09-786-015-4 x AF172687 ..

Align seg 1/1 to: AF172687 from: 1 to: 330
1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
|||||
1 CAGGCTGTGCTGACTCAGCCGCTCTCGTCCGACGCTCGGCGCAGAG 50
|||||
17 gvalserilethrchyserserlyserSerSerAsnIleGlyYAsnAlar 34
|||||
51 TGTCTCATTCACCTGCTCTGGAACAGCAGCAAGCTTGATATGTAATT 100
|||||
34 yrValGlyTrpTyrgLInValProGlySerAlaProArgLeuLeuIle 50
|||||

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101 TTGTGAGCTGTGTACCAACAGGTCCAGAGATCAGCCCCCAATCTTCATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
|||||
151 TTGACACCAACAACTGACCTCGGGGTCCCGCCAGCATTTCTCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84
|||||
201 CAGGCTGTGCGACACACAGCACTGTGACCATCGCTCCCTCCAGGCTGAG 250
84 spGuaIaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
|||||
251 ACGAGCCGATTATTACTGTTCACTTATGACAGCACT...AGCTTTGTA 297
101 PheGlySerGlyThrArgLeuThrValIleuGly 111
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298 TTCGGCAGCGGACCGAGCTGACCTGCTGGGT 330

seq_name: gb_om:AF015798

seq_documentation_block:
LOCUS AF015798 333 bp mRNA linear MAM 10-MAR-2000
DEFINITION Bos taurus immunoglobulin light chain variable region mRNA, partial
cds.
ACCESSION AF015798
VERSION AF015798.1 GI:2323385
KEYWORDS
SOURCE
ORGANISM cow.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 333)
Saint, S.S., Allore, B., Jacobs, R.M. and Kaushik, A.
Exceptionally long CDR3H region with multiple cysteine residues in
functional bovine IgM antibodies
Eur. J. Immunol. 29 (8), 2420-2426 (1999)
JOURNAL MEDLINE
PUBMED 99387993
REFERENCE
2 (bases 1 to 333)
Saint, S.S., Jacobs, R. and Kaushik, A.
Direct Submission
Submitted (24-JUL-1997) Pathobiology, University of Guelph, Guelph,
ON N1G 2W1, Canada
FEATURES
source
1..333
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BLV6D10"
/note="bovine x mouse heterohybridoma secreting IgM
antibody"
<1..>333
/product="immunoglobulin light chain variable region"
/protein_id="AAB6569.1"
/db_xref="GI:2323386"
/translation="QAVLRQPSVSYSGLQQRYSITCSGSSNVGNGNYNMQQIPGS
APRLTIGATSRASGVPDRFSGSRSGNTATLTISLQADEADYFCAAIDSSNNAVF
GSGTTLTVL"
BASE COUNT 64 a 106 c 95 g 68 t
ORIGIN

alignment_scores:
Quality: 440.50 Length: 111
Ratio: 4.277 Gaps: 1
Percent Similarity: 92.793 Percent Identity: 79.279

alignment_block:
US-09-786-015-4 x AF015798 ..

Align seg 1/1 to: AF015798 from: 1 to: 333

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/protein_id="AAB6572.1"
/db_xref="gi:2323392"
/translation="QAVLTQPSVSGSLGQRVSTICSGSSSNVGNVYTWQVPGS
APRFLVGTNRASGVPDRFSGSRSGNTATLTLTSSLDADDEADYFCAYDSSNNAVF
GSGTRLTVLG"
BASE COUNT      64 a      106 c      96 g      67 t
ORIGIN

alignment_scores:
    Quality: 440.50      Length: 111
    Ratio: 4.277      Gaps: 1
    Percent Similarity: 92.793      Percent Identity: 79.279

alignment_block:
US-09-786-015-4 x AF015801 ..

Align seg 1/1 to: AF015801 from: 1 to: 333

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||||||||||||||||||||||||||||||||||||||||||
1 CAGGCTGTGCTGACTCAGCCGCTCTCGGTGTCGGGTCCCTGGGCCAGAG 50
17 GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaAr 34
||||| ||||||||||||||||||||||||||||||||||||||||
51 GGTCTCATTCACCTGCTCTGGAGACAGCAGCAACGTTGGGGGTGCACAT 100
34 yRValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuLeuIle 50
||||| ||||||||||||||||||||||||||||||||||||||||
101 ATGTGAAGCTGTCTCCACACAGATCCAGATCGGCCCCAGAACCTCATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
||||| ||||||||||||||||||||||||||||||||||||||||
151 TATGTGCGACCACTGACGCTCTGGGGTCCCGACCGATTCTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlnA 84
||||| ||||||||||||||||||||||||||||||||||||||||
201 CAGGTCTGGAGACAGCAGCAGCTGACCATTCAGCTCCAGGCCAGAG 250
84 sPgIuaIaAspTyTyrCysAlaSerTyr...GlnSerThrTyrSerGly 99
||||| ||||||||||||||||||||||||||||||||||||||||
251 ACGAGGGGATTAATTTCTGTGACACGCTATGACACAGTACATTAATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 110
||||| ||||||||||||||||||||||||||||||||||||||||
301 GTTTTCGGCAGCGGACACAGCTGACCGCTCCTG 333

seq_name: gb_com:AF172688

seq_documentation_block:
LOCUS      AF172688      336 bp      mRNA      linear      MAM 29-AUG-1999
DEFINITION Ovis aries clone 23 immunoglobulin light chain variable region
            (IGLV) mRNA, partial cds.
ACCESSION      AF172688
VERSION      AF172688.1 GI:5802423
KEYWORDS
SOURCE
ORGANISM      sheep.
                Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 336)
White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
Unpublished
2 (bases 1 to 336)
White,G.P., Meusen,E.N.T. and Newton,S.E.
Direct Submission
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (26-JUL-1999) School of Veterinary Science, The Centre
for Animal Biotechnology, The University of Melbourne, Parkville,
```

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Melbourne, Victoria 3052, Australia
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/db_xref="taxon:9940"
/clone="23"
/tissue_type="abomasal lymph node"
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<1..>336
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CDS
1..336
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/protein_id="AAB51678.1"
/db_xref="gi:5802424"
/translation="QAVLTQPSVSRMGSQSVSTICSGSSSNVGNVYTWQVPGS
APRFLVGTNRASGVPDRFSGSRSGNTATLTLTSSLDADDEADYFCAYDSSNTLNVF
GSGTRLTVLG"
BASE COUNT      68 a      101 c      90 g      77 t
ORIGIN

alignment_scores:
    Quality: 439.50      Length: 112
    Ratio: 4.351      Gaps: 1
    Percent Similarity: 90.179      Percent Identity: 79.464

alignment_block:
US-09-786-015-4 x AF172688 ..

Align seg 1/1 to: AF172688 from: 1 to: 336

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||||||||||||||||||||||||||||||||||||||
1 CAGGCTGTGCTGACTCAGCCGCTCTCGGTGTCGGGTCCCTGACAGTGGGCCAGAG 50
17 GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaAr 34
||||| ||||||||||||||||||||||||||||||||||||||||
51 TGTCTCATTCACCTGCTCTGGAGACAGCAGCAGCATTCGATATGTGTAAT 100
34 yRValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuLeuIle 50
||||| ||||||||||||||||||||||||||||||||||||||||
101 ATGTGAAGCTGTCTCCACACAGATCCAGATCGGCCCCAGAACCTCATC 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
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151 TATGTGCGACCAACTGACGCTCTGGGGTCCCGACCGATTCTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlnA 84
||||| ||||||||||||||||||||||||||||||||||||||||
201 CAGGCTGTGGCCACAGCAGCAGCTGACCATTCAGCTCCAGCTGAGG 250
84 sPgIuaIaAspTyTyrCysAlaSerTyr...GlnSerThrTyrSerGly 99
||||| ||||||||||||||||||||||||||||||||||||||||
251 ACGAGGCCGATTAATTTCTGTGACACGCTATGACACAGTACCTTAATGCT 300
100 ValPheGlySerGlyThrArgLeuThrValLeu 111
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seq_name: gb_com:AF172693

seq_documentation_block:
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DEFINITION Ovis aries clone 64 immunoglobulin light chain variable region
            (IGLV) mRNA, partial cds.
ACCESSION      AF172693
VERSION      AF172693.1 GI:5802433
KEYWORDS
SOURCE
ORGANISM      sheep.
                Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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REFERENCE  
AUTHORS  
TITLE

Bovidae; Caprinae; Ovis.  
1 (bases 1 to 333)  
White,G.P., Meusen,E.N.T. and Newton,S.E.  
A single-chain variable region immunoglobulin library from the  
abomasal lymph node of sheep infected with the gastrointestinal  
nematode parasite Haemonchus contortus

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 333)  
White,G.P., Meusen,E.N.T. and Newton,S.E.  
Direct Submission  
Submitted (26-JUL-1999) School of Veterinary Science, The Centre  
for Animal Biotechnology, The University of Melbourne, Parkville,  
Melbourne, Victoria 3052, Australia

FEATURES  
source

1. .333  
/organism="Ovis aries"  
/db\_xref="taxon:9940"  
/clone="64"  
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/db\_xref="GI:5802434"  
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BASE COUNT  
ORIGIN

64 a 101 c 95 g 73 t

alignment\_scores:  
Quality: 439.00 Length: 111  
Ratio: 4.480 Gaps: 0  
Percent Similarity: 88.288 Percent Identity: 81.081

alignment\_block:  
us-09-786-015-4 x AF172693 ..

Align seg 1/1 to: AF172693 from: 1 to: 333

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1 CAGGCTGTGCTGACTCAGCGCTCCTCCGTCCTCAAGTCCCTGGGCCAG 50
17 gValSerIleThrcysSerGlySerSerAsnIleGlyGlyAsnAlaT 34
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51 GGTCCTCATCTACCTCTCGAGACAGCAGACACGTCGATATGATATA 100
34 yrValGlyTrpTyrGlnValProGlySerAlaProArgLeuLeu 50
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101 ATGTGGGCTGTACCAACAGGTCCAGAGATACCCCAACCTCTCATTT 150
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TATGTGTGAACCGTCGAGCTCGGGGCTCCCGACCGCATCTCCGGCTC 200
67 rArgSerGlyAsnThrAlaThrIleThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CAGTCTGGCAACACAGCAGCTCTGACCATCAGCTCGCTCAGGCTGAG 250
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGly 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 ACGAGCGCGATTATTACTGTGATTTATGACACACGAGTAGTTGGGCTT 300
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 TTGCGCAGCAGACGAGCTGACCGTCTCTGGGT 333
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17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlaIat 34  
|||||  
51 GGTCTCATCACTCTCTGTGACACAGCAGCAACATTGGAGGTATGCTT 100  
34 yValGlyTPryGlnGlnValProGlySerAlaProArgLeuLeuile 50  
|||||  
101 ATGGGGCTGTACCAACAGGTCCAGAGATCAGCCCCAGACTCTCTATTC 150  
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67  
|||||  
151 AGTCTCAACACCGATCGAGCTCGGGGATCCCGACGATTCCTCGGCTC 200  
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84  
|||||  
201 CAGTCTGGGAGAACACAGCACCCCTGACCATCAGCTCGCTCCAGGCTGAG 250  
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100  
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251 ACGAGGCGGATTATTAATGCTGATCGATCAAAAGTACTTACAGTGTGTT 300  
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301 TTGCGCAGCGGAGCAGCAGCTGACCGTCTGCTGCT 333  
seq\_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA158663  
seq\_documentation\_block:  
ID AA158663 standard; cDNA; 585 BP.  
AC AA158663;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 866.  
XX  
KW Human: neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 26-DEC-2000; 2000MO-US34263.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
PA (HYSB-) HYSBQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
DR MPI; 2001-442253/47.  
DR P-PSDB; AAM39507.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT as central nervous system injuries -  
XX  
PS Claim 1; SEQ ID NO 866; 10078bp; English.  
XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and  
CC the encoded polypeptides (AAM38642-AA42213) with neurotropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and inflammation, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemia and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
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SQ Sequence 585 BP; 113 A; 194 C; 156 G; 122 T; 0 other;  
XX  
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Quality: 389.00 Length: 113  
Ratio: 3.814 Gaps: 1  
Percent Similarity: 90.265 Percent Identity: 67.257  
alignment\_block:  
US-09-786-015-4 x AA158663 ..  
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1 GlnAspValIleThrGlnProSerSerValSerGlySerLeuGlyAlaIat 17  
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124 CAGTCTGTGCTGACGACAGCCGCCCTCAGTGTGTGGGGCCCGACGAGAG 173  
17 gValSerIleThrcysSerGlySerSerAsnIleGlyGlyAsnAlaIat 34  
|||||  
174 GGTCTCATCACTCTCTGTGACACAGCAGCAACATTGGAGGTATGCTT 223  
34 yValGlyTPryGlnGlnValProGlySerAlaProArgLeuLeuile 50  
|||||  
224 ATGTACACTGTGTACACAGCACTCCAGGAGACGCCCAAACTCTCATC 273  
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67  
|||||  
274 TATGTTACACAGCAATCGGCCCTCAGGGGTCCCTGACCATTCCTGCTC 323  
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGua 84  
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324 CAAGCTGCGACACTCAGCTCCCTGGCCATCATCTGGCTCCAGGCTGAGG 373  
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGly... 99  
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374 ATGAGGCTGATTATTAATGCTGACGATCGATGACAGAGCTGAGTGTCT 423  
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424 GTGGTATTCGGCGAGGAGCACCATGACCTGACCTCTGAGGT 462  
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seq\_documentation\_block:  
ID AAC6525 standard; cDNA; 935 BP.  
XX  
AC AAC6525;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human immune system associated protein HISP-7 coding sequence.  
XX  
KW Human: immune system associated protein; HISP-7; immune disorder;  
KW infection; autoimmune disease; cancer; ss.  
XX  
OS Homo sapiens.

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XX  US6135941-A.
PN
XX  24-OCT-2000.
PD
XX  27-MAR-1998; 98US-0049672.
XX  27-MAR-1998; 98US-0049672.
XX  27-MAR-1998; 98US-0049672.
XX  (INCYTE) INCYTE PHARM INC.
XX  Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR:
PI  Hillman JL, Au-Young J;
XX  WPI: 2001-030926/04.
DR  P-PSDB; AAB36209.
XX
XX  New human immune system associated proteins (HISAP) and polynucleotides
PT  encoding the HISAP, useful for diagnosing, treating or preventing
PT  immune or cell proliferative disorders or infections
XX
PS  Claim 3; Column 83-84; 54pp: English.
XX
XX  The present invention provides the coding and protein sequences for a
CC  number of human immune system associated proteins (HISAPs). These can be
CC  used in the diagnosis and treatment of various autoimmune disorders,
CC  infections and cell proliferation diseases. The diseases include AIDS,
CC  adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC  Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC  gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC  erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
SQ  Sequence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

alignment_scores:
    Quality: 388.50      Length: 112
    Ratio: 3.847         Gaps: 1
    Percent Similarity: 90.179      Percent Identity: 67.857

alignment_block:
US-09-786-015-4 x AAC66525 ..

Align seg 1/1 to: AAC66525 from: 1 to: 935

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   17 gvalserilethrcyssergylseraseranileglylvasna1at 34
   |||:::|||||:::|||||:::|||||:::|||||:::
181 GCTGCACATCTCCGCACTGGGACAGCTCCACATCGGGGCAAGTATG 230
   34 yValGlyTPYrGlnGlnValProGlySerAlaProArgLeuLeu 50
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231 ATGTACACTGTACACAGCTTCACAGAACGCCCAAACTCCTCATC 280
   51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
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281 TATGGTATGTAATCGCCCTCAGGGGTCCCTGACCGATTCTTGCTC 330
   67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGln 84
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   100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
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XX  AAS77073;
AC
XX  13-FEB-2002 (first entry)
DT
XX  DNA encoding novel human diagnostic protein #12877.
DE
XX  Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW  food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX  Homo sapiens.
OS
XX  WO200175067-A2.
XX  11-OCT-2001.
PD
XX  30-MAR-2001; 2001WO-US08631.
XX  31-MAR-2000; 2000US-0540217.
XX  23-AUG-2000; 2000US-0649167.
XX  (HYSE-) HYSO INC.
XX  Drmanac RT, Liu C, Tang YT;
PI  WPI: 2001-639362/73.
XX  P-PSDB; ABG12886.
DR
XX  New isolated polynucleotide and encoded polypeptides, useful in
PT  diagnostics, forensics, gene mapping, identification of mutations
PT  responsible for genetic disorders or other traits and to assess
PT  biodiversity
XX
XX  Claim 1; SEQ ID NO 12877; 103pp: English.
PS
XX
XX  The invention relates to isolated polynucleotide (I) and
CC  polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC  polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC  and gene mapping, and in recombinant production of (II). The
CC  polynucleotides are also used in diagnostics as expressed sequence tags
CC  for identifying expressed genes. (I) is useful in gene therapy techniques
CC  to restore normal activity of (II) or to treat disease states involving
CC  (II). (II) is useful for generating antibodies against it, detecting or
CC  quantitating a polypeptide in tissue, as molecular weight markers and as
CC  a food supplement. (II) and its binding partners are useful in medical
CC  imaging of sites expressing (II). (I) and (II) are useful for treating
CC  disorders involving aberrant protein expression or biological activity.
CC  The polypeptide and polynucleotide sequences have applications in
CC  diagnostics, forensics, gene mapping, identification of mutations
CC  responsible for genetic disorders or other traits to assess biodiversity
CC  and to produce other types of data and products dependent on DNA and
CC  amino acid sequences. AAS64197-AAS94564 represent novel human
CC  diagnostic coding sequences of the invention.
CC  Note: The sequence data for this patent did not appear in the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ  Sequence 889 BP; 200 A; 293 C; 223 G; 173 T; 0 other;

alignment_scores:
    Quality: 387.00      Length: 111
    Ratio: 3.909         Gaps: 0
    Percent Similarity: 89.189      Percent Identity: 65.766

alignment_block:
US-09-786-015-4 x AAS77073 ..

Align seg 1/1 to: AAS77073 from: 1 to: 889
```

```

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
PS |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX CAGTCTCCCTGACTGACTCAGCTCCCTCCGCGCTCCGCTCTTGACAGTGC 150
17 GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyGlnAlaT 34
151 AGTCACTTCTCTCCGACGTGACACAGCAGTGAATGTAATTAATT 200
34 yValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuIle 50
201 ATGTCCTCCTGTTACCGACACACCCAGGCAAGGCCCAAACTATGATC 250
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
251 TATGAGGTCACTAAGCGGCCCTCAGGGGTCCCTTAACCGCTTCTGCTC 300
67 rArgSerGlyAspThrAlaThrIleThrIleSerSerLeuGlnAlaGUA 84
301 CAACTCTGGCAACAGCGCTCCTGACCGCTCTGGGCTCCAGGCTGAGG 350
84 spGluAlaAspTyTyrCysAlaSerTyrgInserThrTySerGlyVal 100
351 ATGAGGCTGATTATTACTGACAGCTCATACGACGACAGTAATAGTTGATT 400
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
401 TTCGCGGAGGACAGCAGCTGACCGTCTAGT 433

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-embL/NA1992.DAT:AAQ22491
seq_documentation_block:
ID AAQ22491 standard; DNA; 9071 BP.
XX
XX AAQ22491;
XX
DT 31-JUL-1992 (first entry)
XX
DE Human U266 lambda gene.
XX
KW Human myeloma U266 cell line; rearranged lambda gene; Ig;
KW immunoglobulin light chain; pTAR-7; heavy chain enhancer;
KW humoral immunity; transgenic mouse; ATCC No. 72003; ds.
XX
OS Chimeric Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_feature 1..8385
FT /tag= a
FT /note= "U266-lambda gene"
FT misc_feature 8386..9071
FT /tag= b
FT /note= "portion of 995bp XbaI-EcoRI fragment of
FT pTAR-7 contg. mouse H chain enhancer"
XX
XX WO9204440-A.
XX
XX 19-MAR-1992.
XX
XX 27-AUG-1991; 91MO-1006124.
XX
XX 29-AUG-1990; 90US-0575005.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Vasilcek TJ, Leder P;
XX
XX WPI; 1992-114348/14.
XX
XX B cell deficient transgenic non-human animals - comprise DNA
XX encoding the U266 immunoglobulin light chain and an enhancer
XX region used as models of B cell deficiency

```

```

XX
XX Disclosure; Fig 7; 41pp; English.
XX
XX This sequence is the EcoRI/HindIII fragment of the rearranged lambda
CC gene isolated from human myeloma U266 cell line ligated to the mouse
CC heavy chain enhancer. The resulting transgene was used in the
CC production of transgenic mice in which the proportion of spleen cells
CC which are mature B cells is not more than a quarter of that in
CC wild-type animals. The animals are more susceptible to infectious
CC diseases than the wild-type and are models for severe B cell
XX deficiency. See also AAQ22489 for the transgene sequence.
XX
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T; 0 other;

alignment_scores:
Quality: 387.00 Length: 111
Ratio: 3.909 Gaps: 0
Percent Similarity: 89.189 Percent Identity: 65.766

alignment_block:
us-09-786-015-4 x AAQ22491 ..

Align seg 1/1 to: AAQ22491 from: 1 to: 9071

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5440 CAGTCTCCCTGACTGACTCAGCTCCCTCCGCGCTCCGCTCTTGACAGTGC 5489
17 GValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyGlnAlaT 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5490 AGTCACCTTCTCTGACGTGACACAGCAGTGAATGTAATTAATT 5539
34 yValGlyTPTyTGlnGlnValProGlySerAlaProArgLeuIle 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5540 ATGTCCTCCTGTTACCGACACACCCAGGCAAGGCCCAAACTATGATC 5589
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5590 TATGAGGTCACTAAGCGGCCCTCAGGGGTCCCTTAACCGCTTCTGCTC 5639
67 rArgSerGlyAspThrAlaThrIleThrIleSerSerLeuGlnAlaGUA 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5640 CAACTCTGGCAACAGCGCTCCTGACCGCTCTGGGCTCCAGGCTGAGG 5689
84 spGluAlaAspTyTyrCysAlaSerTyrgInserThrTySerGlyVal 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5690 ATGAGGCTGATTATTACTGACAGCTCATACGACGACAGTAATAGTTGATT 5739
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5740 TTCGCGGAGGACAGCAGCTGACCGTCTAGT 5772

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-embL/NA1992.DAT:AAQ23370
seq_documentation_block:
ID AAQ23370 standard; DNA; 9071 BP.
XX
XX AAQ23370;
XX
DT 14-AUG-1992 (first entry)
XX
XX U266-lambda gene and downstream murine Ig Heavy chain enhancer.
XX
XX Lambda-E-mu; rearranged; immunoglobulin; light chain; transgene;
XX B cell deficiency; common variable immunodeficiency; CVID;
XX ATCC # 72003; ds.
XX
XX Chimeric Mus.
XX
XX Chimeric Homo sapiens.
XX
XX WO9204443-A.
XX

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Tue Aug 13 08:57:26 2002

PD 19-MAR-1992.  
XX  
PF 27-AUG-1991; 91MO-US06106.  
XX  
PR 29-AUG-1990; 90US-0575006.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Vasilcek TJ, Leder P;  
XX  
XX WPI; 1992-114351/14.  
DR  
XX B cell deficient transgenic FVB/N mice - comprise DNA encoding  
PT the lambda light chain of a non-human animal for modelling of B  
PT cell deficiency  
XX  
PS Disclosure: Fig 7; 41pp; English.  
XX  
XX DNA from the Ige-lambda human myeloma U266 cell line was digested  
CC with EcoRI and used to prepare a phage library. The clone  
CC containing the active lambda gene was identified by probing the  
CC library with a radiolabelled BamHI fragment of the human lambda 2  
CC gene. (The complete sequence of U266-lambda gene has EMBL Acc. #  
CC X5154). The lambda-E-mu construct was prepared by cutting the  
CC lambda construct at the HindIII site 0.9kb downstream of  
CC C(lambda)2. The fragment was blunt-ended and ligated to a 955bp  
CC XbaI fragment of pRAR-7 containing the mouse Ig heavy chain  
CC enhancer. The transgene construct was used to transfect mouse  
CC cells for the production of B cell deficient transgenic mice. The  
CC mice can be used to study e.g. X-linked agammaglobulinemia.  
XX  
SQ Sequence 9071 BP; 2196 A; 2395 C; 2321 G; 2159 T; 0 other;

alignment\_scores:  
Quality: 387.00 Length: 111  
Ratio: 3.909 Gaps: 0  
Percent Similarity: 89.189 Percent Identity: 65.766

alignment block:

US-09-786-015-4 x AA023370 ..

Align seg 1/1 to: AA023370 from: 1 to: 9071

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17  
5440 CAGCTGCTCCTGACTCAGCTCCCTCCGCGTCCGGTCTTGACAGTC 5489  
17 gvalSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34  
5490 AGTCACCTTCTCCTCGACGTGGAACCAACAGTACATGTGTAATATAT 5539  
34 yrValGlyTrpTyrgInGlnValProGlySerAlaProArGleuLeuIle 50  
5540 ATGTCTCTCTGTCACCGACCAACACCAAGCCCAAGCCCAATCATGATC 5589  
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67  
5590 TATGAGGTCTACTAAGCGCCCTCAGCGGTCCTTAACCGCTTCTTGCTC 5639  
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGluA 84  
5640 CAAGTCTGGCAACACGCGCTCCTGACCCCTCTCGGCTCCAGGCTACG 5689  
84 spGluAlaAspTyrrTyrrCysAlaSerTyrgInSerThrTyrrSerGlyVal 100  
5690 ATGAGCGTGTATTAATCTCAGCTCATACACAGCAGCAATATAGTTGAT 5739  
101 PheGlySerGlyThrArgLeuThrValLeuGly 111  
5740 TTCGGCGGAGGACCAAGCTGACCGTCTTAGGT 5772  
seq\_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: AAS03520

seq\_documentation\_block:  
ID AAS03520 standard; cDNA; 330 BP.

XX AAS03520;

XX 29-AUG-2001 (first entry)

DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 106.

KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;  
KW heart disease; complementarity determining region; CDR; ss.

OS Homo sapiens.

PN WO200127279-A1.

PD 19-APR-2001.

PF 11-OCT-2000; 2000MO-GB03900.

PR 12-OCT-1999; 99US-0158812.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

DR P-PsDB; AA002620.

PT Panel of specific binding members of antibody molecules which bind to  
PT whole adipocytes is used in the treatment of obesity and obesity  
PT related diseases -

PS Disclosure: Page 167; 182pp; English.

XX AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy  
XX and light chain coding sequences of the invention. The antibodies can be  
XX used in the treatment of obesity and obesity related diseases. The  
XX antibodies can be used to deliver drugs or pro-drugs directly to the fat  
XX mass of an obese patient or the antibody can be used as a therapeutic  
XX itself. Antibodies binding specifically to adipocytes can be used to  
XX activate the immune system to destroy the cells by complement mediated  
XX lysis. The antibodies may be labeled with a detectable label such as  
XX radiolabel, fluorescent or chemical group and used in methods of  
XX diagnosis in human subjects e.g. to determine the presence of adipocyte  
XX antigen on the surface of an adipocyte to detect or determine the  
XX presence or level of adipocytes in a cell or tissue sample. The  
XX antibodies can be used as an alternative means of treatment for obese  
XX patients other than undergoing surgery to remove excess fat. Antibodies  
XX for different types of fat deposits can also be produced e.g. intra-  
XX abdominal fat associated with heart disease.

SQ Sequence 330 BP; 69 A; 101 C; 83 G; 77 T; 0 other;

alignment\_scores:  
Quality: 386.00 Length: 110  
Ratio: 3.979 Gaps: 0  
Percent Similarity: 88.182 Percent Identity: 65.455

alignment block:

US-09-786-015-4 x AAS03520 ..

Align seg 1/1 to: AAS03520 from: 1 to: 330

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17  
1 CAGTCTGTGACTCAGCTCCTCGTGTGGTCTCTGACACAGTC 50  
17 gvalSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34  
51 GATCACCATCTCTGACACTGGAACCAACAGTACGATGTGTATTAAGT 100

```
34 yValGIyTPtYrGInGInValProGlySerAlaProArgLeuLeuIle 50
|||||
101 ATGTCTCCTGTACCAACAGCAGCCAGCAAGCCCAACCACTCATGATT 150
51 SerIaThrThraSPArgAlaSerGIyLeProSPArgPheSerGIySe 67
|||||
151 TATGAGGCAATYAAAGCGCCCTCAGGGGTCCCTGATCGCTCTCTGGCTC 200
67 rArgSerGIyAsnThraIaThrLeuThrIleSerSerLeuGInAlaGua 84
|||||
201 CAATCTGTGGCAACAGCGGCTCCCTGACCGTCTCTAGACTCCAGGCTGAGG 250
84 sPGIuaIaAsPTyTyrCysAlaSerTYrGInSerThrTYrSerGIyVal 100
|||||
251 ATGAGGCGTATTATTACTGACGCTCATATGCGACGACGACGAGTGTGCTT 300
101 PheGIySerGIyThraArgLeuThrValLeu 110
|||||
301 TTGCGCGAGGAGGACCAAGCTGACCGTCTTA 330
seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH47733
seq_documentation_block:
ID AAH47733 standard; DNA: 339 BP.
XX
XX AAH47733;
XX
XX 30-NOV-2001 (first entry)
XX
XX Nucleotide sequence of seq id No. 76.
XX
XX Gene library: Immunoglobulin; antibody library; human; ds.
XX
XX Homo sapiens.
XX
XX MO200162907-A1.
XX
XX 30-AUG-2001.
XX
XX 22-FEB-2001; 2001MO-JP01298.
XX
XX 22-FEB-2000; 2000JP-0050543.
XX
XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
XX Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
XX P-PSDB; AAG65369.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
XX light chain that binds to a heavy chain product to produce a functional
XX formation, and producing a gene library of the light chain variable
XX regions -
XX
XX Examples: p 150; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
XX immunoglobulin light and heavy variable region. The method involves
XX selecting light chain that binds with the heavy chain product to produce
XX a functional conformation, producing a gene library comprising a
XX collection of these light chain variable genes, and combining with gene
XX library of heavy chain variable genes. The method is used for production
XX of gene and antibody libraries.
XX
XX Sequence 339 BP; 67 A; 104 C; 95 G; 73 T; 0 other;
XX
alignment_scores:
Quality: 385.00 Length: 113
Ratio: 3.812 Gaps: 1
```

```
Percent Similarity: 89.381 Percent Identity: 67.257
alignment_block:
us-09-786-015-4 x AAH47733 ..
Align seq 1/1 to: AAH47733 from: 1 to: 339
1 GInaSPValLeuThrGInProSerSerValSerGIySerLeuGInArg 17
|||||
1 CAGCGTGTGCTCAGCTCAGCCCTCTCAGTGTCTGTGGGTGCCAGGAGAG 50
17 gValSerIleThrcysSerGIySerSerAsnIleGIyGInaIaT 34
|||||
51 GGTGACCAATCTCCGACCTGGAGGAGAGCTCCACATCGGGGACAGTTATG 100
34 yValGIyTPtYrGInGInValProGlySerAlaProArgLeuLeuIle 50
|||||
101 ATGTACTGTGTACAGCAGCTTCCAGGACAGCCCAACCACTCTCTATC 150
51 SerIaThrThraSPArgAlaSerGIyLeProSPArgPheSerGIySe 67
|||||
151 TATGATACAGCAATYAAAGCGCCCTCAGGGGTCCCTGACGATCTCTGGCTC 200
67 rArgSerGIyAsnThraIaThrLeuThrIleSerSerLeuGInAlaGua 84
|||||
201 CAAGCTGTGGCAACAGCGGCTCCCTGACCGTCTCTAGACTCCAGGCTGAGG 250
84 sPGIuaIaAsPTyTyrCysAlaSerTYrGInSerThrTYrSerGIy... 99
|||||
251 ATGAGCGTGTATTATTACTGCCAGTCTCTATGACAGCAGCTGAGTGTAT 300
100 ..ValPheGIySerGIyThraArgLeuThrValLeuGIy 111
|||||
301 GTGGTATTCTGGCGGAGGAGGACCAAGCTGACCGTCTTACGT 339
seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI68765
seq_documentation_block:
ID AAI68765 standard; DNA: 351 BP.
XX
XX AAI68765;
XX
XX 22-JAN-2002 (first entry)
XX
XX Human autoantibody MICA-6 variable region heavy chain DNA.
XX
XX Autoantigen: fusion protein; islet cell antigen; MICA autoantibody;
XX glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;
XX polyglutandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;
XX variable region; heavy chain; MICA-6; ds.
XX
XX Homo sapiens.
XX
XX EP1149914-A2.
XX
XX 31-OCT-2001.
XX
XX 29-MAR-2001; 2001EP-0107702.
XX
XX 10-APR-2000; 2000DE-1017782.
XX 25-MAY-2000; 2000DE-1025840.
XX (LABO-) LABOR KOCH MERK GMBH.
XX
XX Richter W, Rickert M, Rapp I, Dangel W;
XX WPI; 2001-640702/74.
XX P-PSDB; AAG80216.
XX
XX New fusion protein, useful for diagnosis of diabetes type I and other
XX metabolic diseases, is reactive with autoantibodies against both
XX glutamate decarboxylase and islet cell antigen -
XX
```



XX

3801 GTCTTCGGAAGTGGGACCACGGTCACCGTCTAGGT 336

seq\_name: /STDS1/qcdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH42407



alignment\_scores:                      Quality: 382.00                      Length: 111  
    Ratio: 3.979                      Gaps: 0  
 Percent Similarity: 86.486                      Percent Identity: 64.865

alignment\_block:  
 US-09-786-015-4 x AAC67868 ..

Align seg 1/1 to: AAC67868 from: 1 to: 747

```

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
415 CAGTCCGTCGTGACTCAGCCCTCGCTCGTGGCTCTCTCTGACAGCTC 464
17 gValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
465 GATCACCATCTCCTGCAGTGGACACACAGCAGTGAATGGTGTATTA 514
34 yYValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
515 ATGCTCTGCTGTACCAACACACAGCCAGCAAGCCCAACTCATGATT 564
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
565 TATGAGGCGCAGTACGCGCCCTCAGGGGTTCTAATCGCTTCTGCTC 614
67 rArgSerGlyAsnThrAlaThrIleThrIleSerSerLeuGlnAlaG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
615 CAGGTCTGGCAACACGCGCTCCTCGACAAATCTCGGGCTCAGAGCT 664
84 spGlnAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGly 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
665 ACAGAGCTGATTTATTACTGCAGCTCATATACAAACAGAGACACTG 714
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
715 TTCGCGGAGGACCAAGCTGACCGTCTTAGGT 747

```

seq\_name: /IDS1/gcdata/geneseq/geneseqn-emb1/NA25614.DAT:AA25614

seq\_documentation\_block:

ID AA25614 standard; cDNA; 738 BP.

AC AA25614:

DT 27-MAR-2000 (first entry)

DE Internalising anti-c-erbB-2 receptor antibody scFv F5 cDNA.

KM Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;

KW HER/neu oncogene; tumour-specific; Internalisation; non-immunogenic; ss.

OS Synthetic.

OS Homo sapiens.

Key Location/Qualifiers

FT mat\_peptide 1..738

FT /product= "Internalising anti-c-erbB-2 antibody F5"

PN WO955367-A1.

PD 04-NOV-1999.

PF 23-APR-1999; 99WO-US07395.

PR 24-APR-1998; 98US-0082953.

PR 12-FEB-1999; 99US-0250056.

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Poul MA;

XX

DR WPI: 2000-072168/06.

DR P-PSDB: AAY58235.

PT Novel Internalizing antibodies used to treat cancer cells

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

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XX

XX

XX

alignment\_scores:

Quality: 381.50                      Length: 112  
 Ratio: 3.815                      Gaps: 1  
 Percent Similarity: 89.286                      Percent Identity: 66.964

alignment\_block:

US-09-786-015-4 x AA25614 ..

Align seg 1/1 to: AA25614 from: 1 to: 738

```

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
403 CAGTCTGTGTGACGACGCGCCCTCGAGTGTCTGAGTGGCCGACAG 452
17 gValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
453 GGTACCATCTCTGCACTGAGCAGCTCCAAATCGGGCAGATTATG 502
34 yYValGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
503 GTGTACACTGTGTACACAGCTTCCAGAACACAGCCCAACTCTGATC 552
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
553 TATGTAAACACCAATCGCCCTCAGGGGTCCTACCGATTCTGTGGTT 602
67 rArgSerGlyAsnThrAlaThrIleThrIleSerSerLeuGlnAlaG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
603 CAGTCTGGCAGCTCAGCTCTCGCCCATCTAGGGCTCAGAGCTGAG 652
84 spGlnAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGly... 99
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

653 ATGGGCGCATATTACTGACCCAGTTCTATGACAGCAGCCTAGTGGTGG 702
100 ValPheGlySerGlyThrArgLeuThrValIeuGly 111
|||||:::|||||
703 GTGTTGCGGCGAGGACCAAGCTGACCTGCTAGGT 738
seq_name: /SIBS1/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA503477
seq_documentation_block:
ID AA503477 standard; cDNA; 330 BP.
XX
AC
XX AA503477;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding anti-adipocyte monoclonal antibody light chain, FAT 64.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
XX heart disease; complementarity determining region; CDR, ss.
XX Homo sapiens.
OS
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB03900.
XX
PR 12-OCT-1999; 99US-0158812.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
DR P-PSDB; AAU02577.
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX
PS
PS Disclosure; Page 140-141; 182pp; English.
XX
XX AA503401-AA503535 represent anti-adipocyte monoclonal antibody heavy
and light chain coding sequences of the invention. The antibodies can be
used in the treatment of obesity and obesity related diseases. The
antibodies can be used to deliver drugs or pro-drugs directly to the fat
mass of an obese patient or the antibody can be used as a therapeutic
itself. Antibodies binding specifically to adipocytes can be used to
activate the immune system to destroy the cells by complement mediated
lysis. The antibodies may be labeled with a detectable label such as
radiolabel, fluorescent or chemical group and used in methods of
diagnosis in human subjects e.g. to determine the presence of adipocyte
antigen on the surface of an adipocyte to detect or determine the
presence or level of adipocytes in a cell or tissue sample. The
antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease.
XX
XX Sequence 330 BP; 70 A; 102 C; 82 G; 76 T; 0 other;

alignment_scores:
Quality: 381.00 Length: 110
Ratio: 3.928 Gaps: 0
Percent Similarity: 88.182 Percent Identity: 64.545

alignment_block:
US-09-786-015-4 x AA503477 ..
Align seg 1/1 to: AA503477 From: 1 to: 330

```

[illegible]

CC bound to human serum amyloid protein, to pass through a mammalian  
CC blood brain barrier (BBB). The panel is useful for the selection of  
CC specific binding members with a desired property such as ability to  
CC cross BBB, ability to bind endothelial cells or other brain cell antigen,  
CC ability to bind areas of inflammation in the brain or BBB breakdown or  
CC ability to bind intracellular adhesion molecules and to bind transferrin  
CC receptor. The antibodies are useful in diagnosis, prophylaxis and  
CC treatment of human or animal body, including neurological diseases, such  
CC as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy  
CC and traumatic brain injury and any diseases involving inflammation  
CC occurring within the brain or central nervous system.

xx  
SQ Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 other;

## alignment\_scores:

Quality:	381.00	Length:	111
Ratio:	3.969	Gaps:	0
Percent Similarity:	86.486	Percent Identity:	64.865

## alignment\_block:

US-09-786-015-4 x AAH42401 ..

Align seg 1/1 to: AAH42401 from: 1 to: 333

```
1  GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1  CAGTCTGTGCTGACTCAGCCTGCCTCCGTCTGGGCTCTCTCGACAGTC 50
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlaT 34
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
51 GATCACCATCTCCTGCACTGGAACAGACAGTGTGTGTTATTAAT 100
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
34 yValGlyTyrPtyrGlnGlnValProGlySerAlaProArgLeuIle 50
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
101 ATGTCTCTGTGATCACACACACAGCAAGCCCAACATCATGATT 150
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
   ::: ||| |||::: |||::: |||::: |||::: |||::: |||
151 TATGAGGGCAGTAAGCGCCCTCAGGGGTTTCTAATGCTTCTCTGCTC 200
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
67 fArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
201 CAAGTCTGGCAACACGCGCTCCTGACAAATCTCGGCTCCAGGCTGAGG 250
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
251 ACGAGGCTGATTATTAATCTGACATATACCAACAGGGGCGACTCGAGTT 300
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
301 TTGGCGGAGGAGCAACAGCTGACCTGCTGAGG 333
```

**THIS PAGE BLANK (USPTO)**







Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 83 a 161 c 126 g 97 t

ORIGIN

alignment\_scores:

Quality: 444.50 Length: 112

Ratio: 4.358 Gaps: 1

Percent Similarity: 91.071 Percent Identity: 81.250

alignment\_block:

US-09-786-015-4 x BE590205 ..

Align seg 1/1 to: BE590205 from: 1 to: 467

```

1 GlnaspValleuthrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
74 CAGGCTGCTGACTCAGCCGCTCCTCCGTCGCGGTCCTCGGCGCAGAG 123
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 GGTCCATCAGCTGCTCTGCGACAGCGCAATATGGAAATGGCAATT 173
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yfValGlyTrpTyrgInGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 ATGTAGCTGCTGCCACAGATCCAGAGATGGCCCCAGAGCTGCTATC 223
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TATAGTGGACACTCGAGCCTCTGGGGTCCCGACCGATTCCTCGGCTC 273
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 fArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 CAGGCTGGGACACAGCCACTGACTATCAGCTCGCTCCAGCCGAGG 323
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrrTyrcysAlaSerTyrgInSerThr...TyrSerGly 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 ACGAGCGAGATTATTCTGTGCTCATCTCTGACACTAGTAACAGAGTGT 373
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 AGATTGGGACGGGACACACACTGACCTGCTGCTG 409
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq\_name: gb\_est2:BE485669

seq\_documentation\_block:

LOCUS BE485669 495 bp mRNA linear EST 28-AUG-2000

DEFINITION 172803 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE485669

VERSION BE485669.1 GI:9605202

KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 495)

Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and

Wells,K.D.

REFERENCE

AUTHORS

TITLE

Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

Unpublished (2000)

CONTACT: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -m1nscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGTATGACCAT

BACKWARD: GTTTCACAGTACGACG

Plate: 132 row: F column: 18

Seq primer: ATTAGGTGACTATAG.

Location/Qualifiers

1. 495

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone\_lib="BARC 5BOV"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 95 a 174 c 131 g 95 t

ORIGIN

alignment\_scores:

Quality: 443.00 Length: 111

Ratio: 4.386 Gaps: 0

Percent Similarity: 90.991 Percent Identity: 79.279

alignment\_block:

US-09-786-015-4 x BE485669 ..

Align seg 1/1 to: BE485669 from: 1 to: 495

```

1 GlnaspValleuthrGlnProSerSerValSerGlySerLeuGlyGlnAr 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
87 CAGGCTGCTGACTCAGCCGCTCCTCCGTCGCGGTCCTCGGCGCAGAG 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gValSerIleThrcysSerGlySerSerSerAsnIleGlyGlyAsnAlar 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 GGTCCATCAGCTGCTCTGGAACAGCAGCAAGCTTGGAACTGGCAATT 186
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yfValGlyTrpTyrgInGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
187 TTGTAGCTGGGTCACAGATCCAGAGATGGCCCCAGAGCTGCTATC 236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 TATGCTGGACACTCGAGCCTCGGGTCCCGACCGATTCCTCGGCTC 286
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 fArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGua 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 CAGGCTGGGACACAGCCACTGACCATCAGCTCGCTCCAGCTGAGG 336
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrrTyrcysAlaSerTyrgInSerThr...TyrSerGly 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 ACGAGCGAGATTATTCTGTGCTCATCTTGGCAATTTGTAACAATGCTGT 386
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
387 TTGCGCAGCGGACACACACTGACCTGCTGCTG 419
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

seq\_name: gb\_est2:BE589073

seq\_documentation\_block:

LOCUS BE589073 564 bp mRNA linear EST 28-AUG-2000

DEFINITION 194817 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE589073

VERSION BE589073.1 GI:9842112

KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 564)

Sonstegard,T.S., Capuco,A.V., Van Tassel,J.C.P., Ashwell,M.S. and

Wells,K.D.

REFERENCE

AUTHORS

TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sonstegard TS  
USDA, ARS, Beltsville Agricultural Research Center  
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
Tel: 301 504 8416  
Fax: 301 504 8414  
Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and mismatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 121 row: M column: 18  
Seq primer: ATTGAGTGACACTATAG.

FEATURES  
source Location/Qualifiers

1..564  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 580Y"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 106 a 191 c 155 g 112 t  
ORIGIN

alignment\_scores:  
Quality: 440.00 Length: 111  
Ratio: 4.356 Gaps: 0  
Percent Similarity: 90.991 Percent Identity: 77.477

alignment\_block:

US-09-786-015-4 x BE589073 ..

Align seg 1/1 to: BE589073 from: 1 to: 564

```

1 GlnspvalleuthrGlnProserSerValserGlySerleuGlyGlnar 17
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
100 CAGGCTGTGCTGACACACAGATCCAGATCGGCCCCAGAACCTCATTC 149
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gvalserllethrCysSerGlySerSerSerAnlleGlyGlyAsnAlat 34
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
150 GATCTCCATCACCTGCTGCTGAGAGCAGCAGCAACTGGAAGTGGCAAT 199
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yrvAlGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeuile 50
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
200 ATGTGAGTGTGGTCCACACAGATCCAGATCGGCCCCAGAACCTCATTC 249
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
250 TACGGTGCACCACTGACCCAGCCAGGGGGTCCCGGACGATTCTCCGGCTC 299
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerleuGlnAlaGluA 84
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
300 CAGGCTGTGAGACATAGCACCCTGACCATCAGCTGCTCCAGGGCTGAAG 349
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAla 100
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
350 ACGAGGACGATTATTCTGTGTCATCTTANCAAGGCGTGAAGACACACTGT 399
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 TTCCGGCGGCGGACATACATTCGCTCGGCT 432
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
seq_name: gb_est2:BE476758
```

seq\_documentation\_block:

LOCUS BE476758 496 bp mRNA linear EST 28-AUG-2000  
DEFINITION 160150 BARC 580Y Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BE476758  
VERSION BE476758.1 GI:9596291  
KEYWORDS EST.  
SOURCE  
ORGANISM cow.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 496)

1 Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and

Wells,K.D.

Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@psi.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACGTCACGACG

Plate: 28 row: L column: 3

Seq primer: ATTGAGTGACACTATAG.

FEATURES  
source Location/Qualifiers

1..496  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="BARC 580Y"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."  
BASE COUNT 98 a 167 c 133 g 98 t  
ORIGIN

alignment\_scores:

Quality: 438.00 Length: 112  
Ratio: 4.294 Gaps: 2  
Percent Similarity: 91.071 Percent Identity: 80.357

alignment\_block:

US-09-786-015-4 x BE476758 ..

Align seg 1/1 to: BE476758 from: 1 to: 496

```

1 GlnspvalleuthrGlnProserSerValserGlySerleuGlyGlnar 17
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 CAGGCTGTGCTGACACACATCATCCGTGCTCGGCTCCCGGCGCAGAG 138
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 gvalserllethrCysSerGlySerSerSerAnlleGlyGlyAsnAlat 34
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 GGTCTCCATCACCTGCTGGAAGCAGCAGCAATGTT...GGAATGAT 185
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 yrvAlGlyTrpTyrGlnGlnValProGlySerAlaProArgLeuLeuile 50
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
186 ATGTGAGTGTGGTCCACACAGATCCAGATCGGCCCCAGAACCTCATTC 235
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
236 TATGTGACACAGTCGAGCCTCGGGGGTCCCGGACGATTCTCGGCTC 285
  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerleuGlnAlaGluA 84
```

```

|||||
286 CAGGCTGGGAACACAGCACCCCTGACCATGACTCCTCCAGGCTAGG 335
      84 spgualaaaptyrrtyrcysalaserlyrgln...SerThTySerGly 99
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      336 ACGAGGCGAGTTATTCTGTGCATCTGCTGAGGTAAGTACGATATGCT 385
      100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      386 GTTTTCGGCAGCGGACACACATGACCGCTCCTGGGT 421
seq_name: gb_est2:BG691510

```

## seq\_documentation\_block:

```

LOCUS      BG691510          655 bp    mRNA    linear    EST 02-MAY-2001
DEFINITION 340705 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG691510
VERSION    BG691510.1  GI:13933330
KEYWORDS   EST.
SOURCE     Bos taurus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 655)
AUTHORS   Sonstegard,T.S., Capucio,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
TITLE      Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
JOURNAL    Unpublished (2000)
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCGACGACGACG
            Plate: 99 row: 1 column: 6
            Seq primer: ATTTAGGTGACACTATAG.
            Location/Qualifiers
                source          1..655
                    /organism="Bos taurus"
                    /db_xref="taxon:9913"
                    /clone_lib="BARC 5BOV"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                    Library made from pooled mRNA isolated from mammary
                    tissues at eight physiological, developmental, and disease
                    states."

```

```

BASE COUNT      129 a      221 c      181 g      124 t
ORIGIN

```

## alignment\_scores:

```

Quality: 436.50      Length: 112
Ratio: 4.238          Gaps: 1
Percent Similarity: 91.964      Percent Identity: 78.571

```

## alignment\_block:

```

US-09-786-015-4 x BG691510 ..

```

```

Align seg 1/1 to: BG691510 from: 1 to: 655

```

```

1 GlnAspValLeuThrGlnProSerSerValSerIleSerLeuGlyGlnAr 17
||| |||||||
88 CAGGCTGTGCTGACTCAGCGCTCCTCCGTGCGGCTCCCTGGGCGAG 137

```

```

17 gValSerIleThrCysSerGlySerSerAsnIleGlyCysAlaAr 34
|||||
138 GGTCTCCATCACCTGCTCTGGAGACAGACCAATGTGGAGTGGCAATT 187
      34 yValAlGlyTPPTyrgInGlnValProGlySerAlaProArgLeuLeu 50
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      188 ATGTGAGCTGGTTCACAGATCCAGAGATGGCCCCCAAAATCTCATTC 237
      51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      238 TATGTGTGAGACACTCGAGCCTCTGGGGTCCCGACCGATCTCTCGGCTC 287
      67 rArgSerGlyAsnThrAlaThrIleuThrIleSerSerLeuGlnAlaGua 84
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      288 CAGGCTGGGAACACAGCACCCCTGACCATCAGCTCGCTCCAGCCGAGG 337
      84 spgualaaaptyrrtyrcysalaserlyrgln...SerThTySerGly 99
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      338 ACGAGGCGGATTATTCTGTGATCTCCTGACACTAGTACGAGATT 387
      100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      388 TTTTTCGGCAGCGGACACACACTGACCGTCTGGGT 423
seq_name: gb_est2:BE487574

```

## seq\_documentation\_block:

```

LOCUS      BE487574          493 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 176397 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE487574
VERSION    BE487574.1  GI:9607107
KEYWORDS   EST.
SOURCE     Bos taurus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 493)
AUTHORS   Sonstegard,T.S., Capucio,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
TITLE      Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
JOURNAL    Unpublished (2000)
COMMENT    Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt-trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAT
            BACKWARD: GTTTCCGACGACGACG
            Plate: 138 row: 1 column: 11
            Seq primer: ATTTAGGTGACACTATAG.
            Location/Qualifiers
                source          1..493
                    /organism="Bos taurus"
                    /db_xref="taxon:9913"
                    /clone_lib="BARC 5BOV"
                    /tissue_type="pooled"
                    /lab_host="DH10B"
                    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                    Library made from pooled mRNA isolated from mammary
                    tissues at eight physiological, developmental, and disease
                    states."

```

## FEATURES

## source

```

1..493
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

```

```

BASE COUNT      95 a      173 c      127 g      98 t
ORIGIN

```

## alignment\_scores:

Quality: 435.50 Length: 111  
Ratio: 4.312 Gaps: 1  
Percent Similarity: 90.991 Percent Identity: 77.477

Alignment block:

US-09-786-015-4 x BE487574 ..

Align seg 1/1 to: BE487574 from: 1 to: 493

```
1 GlnaspValleuThrnGlnProSerSerValSerGlySerLeuGlyGlnar 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 CAGGCTGTGTTGACTCAGCCCTCTCCCTGTCCGGGTCCCTGGGCGAG 138
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlat 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 AGTCCCATTCACCTGCTCTGGAGACACATCAGCTCGAAGCTGCAATT 188
34 yValGlyTTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 ATGTGGCTGTGTTCCACACAGATCCAGATCAGCCGCCAGAACCTCATG 238
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 TATGTTGACACAGTCAGCCTCGGGGCTCCCGACCATTTCTCGGCTC 288
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 TACGCTGTGGAGACACAGCCCTGACCATCAGCTCAGCTCGAGGCTGAG 338
84 sPgluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyAl 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
339 ACGAGCGAGATTATTCTGTGATCTTATCAGAGTGT...AATGCTGT 385
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
386 TTGGGACGCGGAGCCACACTGACGCTGCTGGGT 418
```

seq\_name: gb\_est2:BE483566

seq\_documentation\_block:

LOCUS BE483566 518 bp mRNA linear EST 28-AUG-2000  
DEFINITION 169766 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE483566  
VERSION BE483566.1 GI:9603099

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

TITLE Bovidae; Bovinae; Bos.

JOURNAL 1 (bases 1 to 518)

COMMENT Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414

Email: tads@lpsl.barc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCAGCAG

Plate: 23 row: L column: 14

Seq primer: ATTTAGTGTGACACTATAG.

Location/Qualifiers

1..518

/organism="Bos taurus"

/db\_xref="taxon:9913"  
/clone\_lib="BARC 5BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORF6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled mRNA isolated from mammary  
tissues at eight physiological, developmental, and disease  
states."

BASE COUNT 101 a 177 c 141 g 99 t  
ORIGIN

alignment\_scores:  
Quality: 435.00 Length: 112  
Ratio: 4.223 Gaps: 2  
Percent Similarity: 91.964 Percent Identity: 79.464

alignment\_block:

US-09-786-015-4 x BE483566 ..

Align seg 1/1 to: BE483566 from: 1 to: 518

```
1 GlnaspValleuThrnGlnProSerSerValSerGlySerLeuGlyGlnar 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
92 CAGGCTGTGTTGACTCAGCCATCATCCGTCCGGGTCCCTGGGCGAG 141
17 gValSerIleThrCysSerGlySerSerSerAsnIleGlyGlyAsnAlat 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
142 GGTCCCATTCACCTGACCGGAGACAGCAATGTT...GGAATGAT 188
34 yValGlyTTrpTyrGlnGlnValProGlySerAlaProArgLeuLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 ATGTGACCTGTGTTCCACACAGATCCAGATGAGGCCGCCAGAACCTCATC 238
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlySe 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
239 TATGTTGACACAGTCAGCCTCGGGGCTCCCGACCATTTCTCGGCTC 288
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlu 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
289 CAGGCTGTGGAGACACAGCCCTGACCATCAGCTCAGCTCGAGCTGAG 338
84 sPgluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSer...Gly 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
339 ACGAGCGAGATTATTCTGTGATCTTATCAGAGTGT...AATGCTGT 388
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
389 GTTTTGGCAGCGGAGCCACACTGACCTGCTGGGT 424
```

seq\_name: gb\_est2:BE231054

seq\_documentation\_block:

LOCUS BE231054 363 bp mRNA linear EST 14-NOV-2000  
DEFINITION 253265 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE231054

VERSION BE231054.1 GI:11169668

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

TITLE Bovidae; Bovinae; Bos.

JOURNAL 1 (bases 1 to 363)

COMMENT Mapping of Expressed Sequence Tags from a normalized bovine mammary

gland cDNA library

Unpublished (2000)

Contact: Sonstegard TS

USDA, ARS, Beltsville Agricultural Research Center

Bldg. 200 Rm 2A, Beltsville, MD 20705, USA

Tel: 301 504 8416

Fax: 301 504 8414  
 Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
 and -mismatch 12 options.

PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTACAGAG  
 Plate: 107 row: D column: 2  
 Seq primer: ATTTAGTGACACTATAG.  
 Location/Qualifiers

## FEATURES

source  
 1..363  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC 5BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."

BASE COUNT 70 a 109 c 101 g 83 t  
 ORIGIN

alignment\_scores:  
 Quality: 426.50 Length: 114  
 Ratio: 4.181 Gaps: 1  
 Percent Similarity: 89.474 Percent Identity: 75.439

alignment\_block:  
 US-09-786-015-4 x BF231054 ..

Align seg 1/1 to: BF231054 from: 1 to: 363

```

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAT 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
19 CAGGCTGCTGCTGACTCAGCCGCGCTCGGCTCGGCTCGGCGCAG 68
17 gvalserilethrcyserserSerSerAsnIleGlyAsnAlaAT 34
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 GGTCTCATACCTGCTCTGGAAGCAGACCATGTTGGATACGGCAAT 118
34 yValAlaGlyTPTyrgInGlnValProGlySerAlaProArgLeuLeu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
119 ATGTGAGCTGTGTCCAAAGATCCAGAGTCGCGCCCGAGAAATGCTAAT 168
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
::: ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
169 TATGATGTAACCACTCGAGCCTCGGGGTCGCCGACGATTCCTCGGCTC 218
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGln 84
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
219 CAGGTCTGGGAACACAGCCATCAACATCACTCGCTCCAGCGCAGG 268
84 spGluAlaAspTyrTyrgCysAlaSerTyrgInSerThrTyrSer.... 98
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
269 ACGAGCGCGATTTATTTCTGTGATCTCTGACAGTAGTAGTAGTAGCT 318
99 ... GlyValPheGlySerGlyThrArgLeuThrValLeuGly 111
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
319 GTTGTGCTTTTCGGCGGGGACCATATTGACCGCTCTGGGT 360

```

seq\_name: gb\_est2:BG692788

seq\_documentation\_block:

LOCUS BG692788 491 bp mRNA linear EST 02-MAY-2001  
 DEFINITION 342607 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BG692788  
 VERSION BG692788.1 GI:13934608  
 KEYWORDS EST.  
 SOURCE COV.  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Mapping of Expressed Sequence Tags from a normalized bovine mammary  
 gland cDNA library  
 Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200, Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -mnscore 18  
 and -mismatch 12 options.

PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTACAGAG  
 Plate: 43 row: F column: 6  
 Seq primer: ATTTAGTGACACTATAG.  
 Location/Qualifiers

## FEATURES

source

1..491  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC 5BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."

BASE COUNT 101 a 167 c 131 g 92 t  
 ORIGIN

alignment\_scores:  
 Quality: 423.00 Length: 112  
 Ratio: 4.147 Gaps: 2  
 Percent Similarity: 91.071 Percent Identity: 76.786

alignment\_block:  
 US-09-786-015-4 x BG692788 ..

Align seg 1/1 to: BG692788 from: 1 to: 491

```

1 GlnAspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnAT 17
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 CAGGCTGCTGCTGACTCAGCCATCATTCGTCGCGGCTCGCTCGGCGCAG 142
17 gvalserilethrcyserserSerSerAsnIleGlyAsnAlaAT 34
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
143 GGTCTCATACCTGCTCTGGAAGCAGACCAATGTT...GGAATGAT 189
34 yValAlaGlyTPTyrgInGlnValProGlySerAlaProArgLeuLeu 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
190 ATGTGAGCTGTACCAACATGATCCAGCTCGGCCCGACAGACCTGATA 239
51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
240 TATGATGACCAATCGCGCTCGGGGTCGCCGACGATTCCTCGGCTC 289
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGln 84
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
290 CAGGTCTGGGAACACAGCCATCAACATCACTCGCTCCAGCGTAGG 339
84 spGluAlaAspTyrTyrgCysAlaSerTyr...GlnSerThrTyrSerGly 99
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
340 ACGAGCGAGATTTATTTCTGTGAGCTCTGACATATACAAATAATGCT 389
100 ValPheGlySerGlyThrArgLeuThrValLeuGly 111

```

```

:::|||||
390 CTTTTCGCGCGGACACACACTGACCTGCTGGCT 425
seq_name: gb_est2:BG689524

```

```

seq_documentation_block:
LOCUS      BG689524                484 bp    mRNA    linear    EST 02-MAY-2001
DEFINITION 337633 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BG689524
VERSION     BG689524.1  GI:13931325
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 484)
            Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
            Wells,K.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
            Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAAT
            BACKWARD: GTTTCACGTCACGACG
            Plate: 102 row: K column: 2
            Seq primer: ATTTAGTGACACTATAG.

```

```

FEATURES
    source
        1..484
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="BARC 5BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: PCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
            Library made from pooled mRNA isolated from mammary
            tissues at eight physiological, developmental, and disease
            states."

```

```

BASE COUNT      86 a      161 c      136 g      101 t
ORIGIN

```

```

alignment_scores:
    Quality: 414.00      Length: 111
    Ratio: 4.099        Gaps: 0
    Percent Similarity: 90.991      Percent Identity: 72.072

```

```

alignment_block:
US-09-786-015-4 x BG689524 ..

```

```

Align seg 1/1 to: BG689524 from: 1 to: 484

```

```

1 GlnAspValLeuThrGlnProSerSerValSerIleuGlyGlnAr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 CAGCGCTGTACTGACTCAGCCCTCTCCGTGTCGCGGTCGCCGCGCAGAG 142
17 gValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAla 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
143 GGTTCATCATCCTGCTCTGGAGCAGGAGCAATGTTGGACTTGGCAATG 192
34 yrValGlyTPTyGInGlnValProGlySerAlaProArgLeuLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 ATGTGAGTTGGTTCCACAGATCCAGATGGGCCCAAAATGTCATC 242

```

```

51 SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGly 67
   ::::: ||| ||| ||||| ||||| ||||| ||||| |||||
243 TATGTCGACACAGACACACCTCTGGGGGTCCCGACCATTCCTCCGGCTC 292
67 rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaIua 84
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
293 CAGGTCGTGGAGACACACACCCCTGACCATCATGCTCCAGGCGGAGG 342
84 spGluAlaAspTyrTyrcysAlaSerTyrGlnSerThrTyrsGlyVal 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
343 ACGAGCGGAGTATTTTGTTCATCTCTCCATGATGATAGCGGATAT 392
101 PheGlySerGlyThrArgLeuThrValLeuGly 111
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
393 TTGCGCGCGGACACACACTAAGCGTCTGGCT 425
seq_name: gb_est2:BE476453

```

```

seq_documentation_block:
LOCUS      BE476453                489 bp    mRNA    linear    EST 28-AUG-2000
DEFINITION 159697 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BE476453
VERSION     BE476453.1  GI:9595986
KEYWORDS   EST.
SOURCE     cow.
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 489)
            Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
            Wells,K.D.
            Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
            Unpublished (2000)
            Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@psi.barc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -mnscore 18
            and -mismatch 12 options.
            PCR Primers
            FORWARD: AGGAACAGCTATGACCAAT
            BACKWARD: GTTTCACGTCACGACG
            Plate: 27 row: I column: 22
            Seq primer: ATTTAGTGACACTATAG.

```

```

FEATURES
    source
        1..489
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="BARC 5BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: PCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
            Library made from pooled mRNA isolated from mammary
            tissues at eight physiological, developmental, and disease
            states."

```

```

BASE COUNT      87 a      174 c      130 g      98 t
ORIGIN

```

```

alignment_scores:
    Quality: 413.50      Length: 112
    Ratio: 4.177        Gaps: 1
    Percent Similarity: 88.393      Percent Identity: 75.893

```

```

alignment_block:
US-09-786-015-4 x BE476453 ..

```

```

Align seg 1/1 to: BE476453 from: 1 to: 489

```

```

1 GlnAspValLeuThrGlnProSerSerValSerIleuGlyGlnAr 17
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
93 CAGCGCTGTACTGACTCAGCCCTCTCCGTGTCGCGGTCGCCGCGCAGAG 142
17 gValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAla 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
143 GGTTCATCATCCTGCTCTGGAGCAGGAGCAATGTTGGACTTGGCAATG 192
34 yrValGlyTPTyGInGlnValProGlySerAlaProArgLeuLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
193 ATGTGAGTTGGTTCCACAGATCCAGATGGGCCCAAAATGTCATC 242

```

```

1  GlnaspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnar 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
75  CAGTCTGTGTGACTCAGCGCTCTCCGTCTCGGGTCCCTGGGCCAGAG 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
125  GGTCTCATCATCCTGCTGTGAGACGCGTCACAGCTGGAGCTGACATTT 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  yrValAlaGlyPtyrGlnGlnValProGlySerAlaProArgLeuIle 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
175  ATGTGAGCTGTTCACACAGATCCAGAGTCGCCCCACAAACCCATCATC 224
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
225  TATGTGCGCACACGAGCGCTCGGGGATCCCGACCGATTCCTCCGGCTC 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlna 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
275  CAGTGGGGGACACAGCCACCTGACGATCGCTCGCTCCAGGCTGAGG 324
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
325  ACGAGCGACGCTACTTGTGTGATCTGCTCAGATCGGCAATGCTGCTGT 374
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  ...PheGlySerGlyThrArgLeuThrValLeuGly 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
375  GCTTTCGGCAGCGGACCACTGTGAACGTCTCGGT 410

```

seq\_name: gb\_est2:BG688615

seq\_documentation\_block:

LOCUS BG688615 528 bp mRNA linear EST 02-MAY-2001  
 DEFINITION 363301 BARC SBOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BG688615  
 VERSION BG688615.1 GI:13930416  
 KEYWORDS EST.  
 SOURCE cov.  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 528)  
 Sonstegard,T.S., Capucio,A.V., Van Tassel,J.C.P., Ashwell,M.S. and  
 Wells,K.D.

REFERENCE  
 AUTHORS Mapping of Expressed Sequence Tags from a normalized bovine mammary  
 gland cDNA library  
 Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

TITLE  
 JOURNAL Mapping of Expressed Sequence Tags from a normalized bovine mammary  
 gland cDNA library  
 Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

COMMENT  
 Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -m1nscore 18  
 and -m1nmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCCAGTACGACG  
 Plate: 104 row: L column: 2  
 Seq primer: ATTGAGTACACTATG.

FEATURES  
 Location/Qualifiers  
 1..528  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC SBOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."

BASE COUNT 102 a 187 c 139 g 100 t  
 ORIGIN  
 alignment\_scores:  
 Quality: 413.50 Length: 111  
 Ratio: 4.177 Gaps: 1  
 Percent Similarity: 89.189 Percent Identity: 73.874

alignment\_block:  
 us-09-786-015-4 x BG688615 ..

Align seg 1/1 to: BG688615 from: 1 to: 528

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1  GlnaspValLeuThrGlnProSerSerValSerGlySerLeuGlyGlnar 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
90  CAGCTGTGCTGACTCAGCGCTCTCCGTCTCGGGTCCCTGGGCCAGAG 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yValSerIleThrCysSerGlySerSerAsnIleGlyGlyAsnAlar 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140  GGTCTCATCATCCTGCTGTGAGACGCGTCACAGCTGGAGCTGACATTT 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  yrValAlaGlyPtyrGlnGlnValProGlySerAlaProArgLeuIle 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
187  ATGTGAGCTGTTCACACAGATCCAGAGTCGCCCCACAAACCCATCATC 236
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  SerAlaThrThrAspArgAlaSerGlyIleProAspArgPheSerGlyse 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
237  TATGGAGTAGACAGCGCACCGCTCGGGGATCCCGACCGATTCCTCCGGCTC 286
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rArgSerGlyAsnThrAlaThrLeuThrIleSerSerLeuGlnAlaGlna 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
287  CAGTGGGACACACAGCCACCTGACGATCGCTCGCTCCAGGCTGAGG 336
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  spGluAlaAspTyrTyrCysAlaSerTyrGlnSerThrTyrSerGlyVal 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
337  ACGACAGGATTAATCTGTGCAACGTATGACACTAGACTACTATTT 386
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  PheGlySerGlyThrArgLeuThrValLeuGly 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
387  TTCGGCAGCGGACCACTGTGAACGTCTCGGT 419

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seq\_name: gb\_est2:BE588329

seq\_documentation\_block:

LOCUS BE588329 474 bp mRNA linear EST 28-AUG-2000  
 DEFINITION 194153 BARC SBOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BE588329  
 VERSION BE588329.1 GI:9841368  
 KEYWORDS EST.  
 SOURCE cov.  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 474)  
 Sonstegard,T.S., Capucio,A.V., Van Tassel,J.C.P., Ashwell,M.S. and  
 Wells,K.D.

REFERENCE  
 AUTHORS Mapping of Expressed Sequence Tags from a normalized bovine mammary  
 gland cDNA library  
 Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

TITLE  
 JOURNAL Mapping of Expressed Sequence Tags from a normalized bovine mammary  
 gland cDNA library  
 Unpublished (2000)  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

COMMENT  
 Email: tads@psi.barc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -m1nscore 18  
 and -m1nmatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCCAGTACGACG

FEATURES  
 Location/Qualifiers  
 1..474  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_lib="BARC SBOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: PCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
 Library made from pooled mRNA isolated from mammary  
 tissues at eight physiological, developmental, and disease  
 states."







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BASE COUNT      78 a      112 c      96 g      83 t
ORIGIN

alignment_scores:
    Quality: 453.00      Length: 124
    Ratio: 4.118      Gaps: 2
    Percent Similarity: 88.710      Percent Identity: 74.194

alignment_block:
US-09-786-015-2 x AF172680 ..

Align seg 1/1 to: AF172680 from: 1 to: 369

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGGTCAACTGCAGAGATCGGGACCCACCTGATGAAACCTCTCAGAC 50
17 rleuSerLeuThrGlySThrValSerGlyPheSerLeuThrLysTYrGlyV 34
|||||
51 CCTGTCCTCCACCTGCTGGTCTGTGATTCATTAACCACTATAGTG 100
34 alserTYrValArgGlnAlaProGlyLysAlaLeuGlnUtrPheuglygly 50
|||
101 TAGTCTGGTCCGCCAGCGCTCCAGAAAGCACTGGAGTGGGTGGTGC 150
51 ValSerSerGlyAlaLeuThrAlaTyrsnThrAlaLeuGlnSerArgle 67
::: ||| ::::: ||||| |||||::: |||||
151 ATATATAGTATGATGAAGTGCATCTATTAACCGCGCTGAAATCCCGGCT 200
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLysSer 84
|||||
201 CAGCGTCACACAGGACACCTCCAGAGCCAGCAAGTCTCCGTCACTAGCA 250
84 eValThrThrGlnLusPThrAlaAlaLeTYrCysAlaLys..... 97
|||||
251 GGGTGACACACTGAGGACACGGCCGTGTACTGTCTGTAGAGACCGTTT 300
|||||
98 SerValasnGlyAspSerValProTYrGlyLeuAspTYrTTPSerProG 114
|||||
301 AGTGCTATGATGATCAGCTTAT...CTGTCCATMGACTACTGGGCGCCAG 347
114 yleuLeuThrValSerSer 121
|||||
348 ACTCCGTGTCACCGTCTCTCA 369

seq_name: gb_cm:AF172662

seq_documentation_block:
LOCUS AF172662 345 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 17 immunoglobulin heavy chain precursor (IGHV)
ACCESSION AF172662
VERSION AF172662.1 GI:5815193
KEYWORDS
SOURCE
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
AUTHORS 1 (bases 1 to 345)
TITLE White,G.P., Meusen,E.N.T. and Newton,S.E.
A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 345)
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
JOURNAL Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
location/Qualifiers
FEATURES

```

```

source
1. .345
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="17"
/issue_type="abomasal lymph node"
/notes="Isolated from animals infected with Haemonchus contortus"
1. .345
/gene="IGHV"
1. .345
/gene="IGHV"
1. .345
/gene="IGHV"
<1. .345
/gene="IGHV"
/codon_start=1
/product="immunoglobulin heavy chain precursor"
/protein_id="A052589.1"
/db_xref="GI:5815194"
/translation="OYLOESGPSLVKPSQSLTICTVSGFSITNYGVQVWVQAPG
KALEMIGTIVSGSFTYYPALKPRLSITRDTKSGVSLSSVTEDTAVYCKRNG
DYGPGILVTYSS"

BASE COUNT      82 a      102 c      94 g      67 t
ORIGIN

alignment_scores:
Quality: 451.00      Length: 123
Ratio: 4.337      Gaps: 3
Percent Similarity: 84.553      Percent Identity: 76.423

alignment_block:
US-09-786-015-2 x AF172662 ..

Align seg 1/1 to: AF172662 from: 1 to: 345

1 GlnValGlnLeuGlnIuSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCAACTGCAGAGTCGGAGACCAGCTGGTGAAGCCCTCACAGAC 50
17 flueSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyr... 32
|||||
51 CCTCTCCCTCACCTGCACAGGCTCTGCACTCTCAATACCACTATGGTG 100
33 ..GlyValSerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeu 48
|||||
101 TTGGTGGAGACTGGGTCCGCCAGGCTCCAGGAAGGACCTGAGATGGTT 150
49 GlyGlyValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGln 65
|||||
151 GGTACCATATATAGTGGTGAAGTACATACATAACCCGCCCTGAAACC 200
65 fArgLeuSerValThrArgAspThrSerLysSerGlnPheSerLeuSerL 82
|||||
201 CCGGCTCAGCATCACACAGGACACTACCAAGACCAAGTCTCCCTGTCAT 250
82 euserSerValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSer 98
|||||
251 TGACACAGGTAAACAACGAGACACGGCCGTACTACTGT...AAGGA 297
99 ValAsnGlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLe 115
|||||
298 GGAATATGC.....GACTACTGGGGCCAGGACT 326
115 uleuLeuThrValSerSer 121
|||||
327 CCTGTACACGCTCTCTCA 345

seq_name: gb_om:OAVRB71G
seq documentation block:
LOCUS OAVRB71G 429 bp mRNA linear MAR 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRB7).
ACCESSION 249193

```

```

VERSION 249193.1 GI:794139
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 429)
AUTHORS Dufour V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMIG, 40, avenue du Recteur Plineau, Poitiers, FRANCE, 86022
AUTHORS Dufour V. and Nau F.
TITLE Sheep immunoglobulin mu heavy chain variable region sequence
JOURNAL Unpublished
FEATURES
source location/Qualifiers
1. .429
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VRB7"
/issue_type="spleen"
/rearranged
1. .429
/gene="VH"
1. .429
/gene="VH"
1. .429
/gene="VH"
1. .429
/gene="VH"
/codon_start=1
/product="VH region precursor"
/protein_id="CAA89052.1"
/db_xref="GI:794140"
/translation="NKPWLTLFVLISAPRGVLQVRLQESGPSLVKPSQSLTICTV
SGFSITVNAVGVWQAPGKYPWELGISTIDGSTYNALSKRLSITRDTKSGVSLSS
SVTTEDTAVYCCARTRFSGGFAVGNIDYWGPGILVTYSS"

sig_peptide
V_region
D_segment
BASE COUNT      89 a      132 c      117 g      91 t
ORIGIN

alignment_scores:
Quality: 450.50      Length: 124
Ratio: 4.095      Gaps: 1
Percent Similarity: 88.710      Percent Identity: 73.387

alignment_block:
US-09-786-015-2 x OAVRB71G ..

Align seg 1/1 to: OAVRB71G from: 1 to: 429

1 GlnValGlnLeuGlnIuSerGlyProSerLeuValLysProSerGlnTh 17
|||||
58 CAGGTGCGGCTGCAGAGTCCGGAGCCAGCTGGTGAAGCCCTCACAGAC 107
17 flueSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
108 CCTCTCCCTCACCTGCACAGGCTCTGCACTCTCAATACCGTCAATGGTG 157
34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGly 50
|||||
158 TAGCGTGGGTCCGCCAGGCTCCAGGAAGGTGCCGAGATGGTGTGATG 207
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67.
|||||
208 ATAAGCACTGATGAAGCAAGCAAGTAAACCGGCCCTGAATATCCGGCT 257

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V_region      349..426      /note="CDR3"
V_region      427..459      /note="FR4"
C_region      460..>462
BASE COUNT    86 a      132 c      138 g      106 t
ORIGIN

alignment_scores:
      Quality: 446.50      Length: 134
      Ratio: 4.059      Gaps: 2
Percent Similarity: 82.090      Percent Identity: 70.149

alignment_block:
US-09-786-015-2 x BRU55202      ..

Align seg 1/1 to: BTU55202 from: 1 to: 462

1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
58  CAGGTGACAGCTCGCGGAGTCGGGCCCGCTGGTGAACCCCTCACAGAC 107
17  rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
108  CCTGTCCTCCACCTGCACGCTCTGTGATTCTCATTTGACACGCTAGGG 157
34  aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
|||||
158  TAGGGCTGGGTCGCCGACAGCTCCAGGGGAAGCGCTGGAGTGTGTGT 207
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
208  ATAAAGTAGGTGGTGAAGCACAGCTATATATCCAGCCCTTGAAATCCCG 257
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
258  CAGCATCACCAAGACAACTCCAAAGGCCAATTCCTCTGTCTACGTAGCA 307
84  eValThrThrGlnLyspThrAlaIleTyrTyrCysAlaLys..... 97
|||||
308  GGGTGCACATTGAGGACACAGCGCCACATACTACTGTGCGAAGAGTGTGT 357
98  .....SerValAsnGlyAspSerValProTyrGly..... 107
|||||
358  TATGCTAGTCAGATGCTGACGTTGTGCCAACTGGGAGTGGTGTGTTTC 407
108  .....LeuAspTyrTrpSerProGlyLeuLeuLeuThrValSerS 121
408  TGGTTGTGTGCGTGCATGCTGGGGCCAAAGAGCTCCTGTGACCGTCTCT 457
121  er 121
||
458  CA 459

seq_name: qb_cm:OAVR3IG

seq_documentation_block:
LOCUS      OAVR3IG      453 bp      mRNA      linear      MAM 04-FEB-1998
DEFINITION      O.aries mRNA for immunoglobulin mu heavy chain variable region
               (clone VR3) .
ACCESSION      249161
VERSION      249161.1 GI:794111
KEYWORDS      diversity region; immunoglobulin; immunoglobulin heavy chain;
               joining region; variable region.

SOURCE
ORGANISM      sheep.
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 453)
Dufour,V.
Direct Submission

```

JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA 1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022

REFERENCE 2 (bases 1 to 453)

AUTHORS Dufour V., Malinge S. and Nau F.

TITLE The sheep Ig variable region repertoire consists of a single VH family

JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)

MEDLINE 96310953

FEATURES

source Location/Qualifiers

1..453

/organism="Ovis aries"

/db\_xref="taxon:9940"

/clone="VR3"

/tissue\_type="spleen"

/rearranged

31..453

gene /gene="VH"

31..>453

/gene="VH"

/codon\_start=1

/product="VH region precursor"

/protein\_id="CA89030.1"

/db\_xref="GI:794112"

/translation="MNPMLTFLVLSAPRGVLSQVQLQESGPVLKPSQTLSLTCTVS  
GFSLSNAVGMWRQAPKALEWVGFYTRGSIYNPAMKSRISITRDKSKQVSLTSL  
SVTDEDTAVVYCARDSGYAYGCSIDYWGPELTVTS"

31..81

sig\_peptide /gene="VH"

82..453

/gene="VH"

/product="VH region"

379..453

/gene="VH"

/note="D-JH region"

BASE COUNT 95 a 139 c 119 g 100 t

ORIGIN

alignment\_scores:

Quality: 444.50 Length: 123

Ratio: 4.116 Gaps: 2

Percent Similarity: 87.805 Percent Identity: 73.171

alignment\_block:

US-09-786-015-2 x OAVR3IG ..

Align seg 1/1 to: OAVR3IG from: 1 to: 453

1 GlnValGlnLeuGlnGlnUserGlyProSerLeuValLysProSerGlnTh 17

|||||

88 CAGGTGACAGTCGACGAGTCGGGACCCAGCTGGTGAAGCCCTCACAGAC 137

17 rLeuSerLeuThCysThrValSerGlyPheSerLeuThLysTyGlyV 34

|||||

138 CCTCTCCCTCACCTGCACGCTCTCTGATTCTCATTAACGACGAAATGCTG 187

34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGlyGly 50

|||||

188 TAGCGTGGGCGCCAGCGCTCCAGAAAGCAGCAGCTGGGCTGGTTTC 237

51 ValSerSerGlyAlaLeuThrAlaTyPheThrValAlaLeuGlnSerArgLe 67

|||||

238 ATATATATCTGAGGAGACATATATACCCGCCCATGAATCCCGGCT 287

67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSerS 84

|||||

288 CAGATATACACAGGACACCTTAAGAGCCAAAGTCTCCCTGACATGAGACA 337

84 eValThrThrGlnAspThrAlaLeuTyPheCysAlaLysSerValAsn 100

|||||

338 GCGTGACAACTGAGGACACGCGCTGACTACTGTGCAAGAGAT...AGT 384

101 GlyAspSerValProTyGly.....LeuAspTyTrpSerProGlyLe 115

|||||

385 GGTATGCTATGCTATGCTGCTGCATCGACATCTGCGGCGCCAGGACT 434

115 uLeuLeuThrValSerSer 121

|||||

435 CCTGCTCACCTCTCTCTCA 453

seq\_name: gb\_om:BT049773

seq\_documentation\_block:

LOCUS BT049773 486 bp mRNA linear MAY 16-AUG-2001

DEFINITION Bos taurus immunoglobulin rearranged heavy chain variable region

RNA, partial cds.

ACCESSION U49773

VERSION U49773.1 GI:1293591

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.

REFERENCE 1 (bases 1 to 486)

AUTHORS Berens,S.J., Wylie,D.E. and Lopez,O.J.

TITLE Use of a single VH family and long CDR3s in the variable region of cattle Ig heavy chains

JOURNAL Int. Immunol. 9 (1), 189-199 (1997)

MEDLINE 97196871

PUBMED 9043960

REFERENCE 2 (bases 1 to 486)

AUTHORS Berens,S.J., Wylie,D. and Lopez,O.J.

TITLE Direct Submission

JOURNAL Submitted (22-FEB-1996) Osvaldo J. Lopez, Biological Sciences, University of Nebraska, 325 Manter Hall, Lincoln, NE 68588-0118, USA

FEATURES

source Location/Qualifiers

1..486

/organism="Bos taurus"

/db\_xref="taxon:9913"

/cell\_type="heterohybridoma"

/tissue\_type="spleen"

/dev\_stage="adult"

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/codon\_start=1

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/protein\_id="AA98654.1"

/db\_xref="GI:1293592"

/translation="LRQLRQGVYVTLTKSKMNPMLTFLVLSAPRGVLSQVQLQESGP  
SLVKPSQTLSTCTISGFSLSYGVMMWRQAPKALEKLGISGGNTGPNPAKSRSL  
SITKDKMSQVLSVSVTPEDTATYCAKSSLGWAGYGTIDYQSYCVDWAGQGLTVV  
SS"

BASE COUNT 104 a 143 c 131 g 108 t

ORIGIN

alignment\_scores:

Quality: 444.00 Length: 129

Ratio: 4.111 Gaps: 2

Percent Similarity: 83.721 Percent Identity: 71.318

alignment\_block:

US-09-786-015-2 x BT049773 ..

Align seg 1/1 to: BT049773 from: 1 to: 486

1 GlnValGlnLeuGlnGlnUserGlyProSerLeuValLysProSerGlnTh 17

|||||

106 CAACTGACAGTCGCGAGATCGGGCCAGCCTGGTGAAGCCCTCACAGAC 155

17 rLeuSerLeuThCysThrValSerGlyPheSerLeuThLysTyGlyV 34

|||||

156 CCTCTCCCTCACCTGCACGATCTGGAATCTCATTTGACGACTATGGTGG 205

34 aLseTrpValArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGlyGly 50

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|||||
206 TAACTGGGTCGCCAGGCTCCAGGAGGCGCTGAGTGCCTGCTGCT 255
51 ValSerSerGlyAlaLeuThrAlaTyrAspThrAlaLeuGlnSerArgLe 67
   |||
256 ATAGCAGCTGGTGGAAACACAGGCTATACCCAGCCCTGAAATCCCGGCT 305
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
   |||
306 CAGCATCAACAGGACCACTCCAGAGCCAGTCTCTCTGTCAGTGACCA 355
84 eValThrThrGluAspThrAlaLeuTyrTyrGlyAlaLeuSerValAsn 100
   |||
356 GCGTGACACCTGAGGACACGGCCACTACTGTCGCAAAAAGTTCTCTT 405
101 GlyAspSerValProTyrGlyLeuAspTyr..... 110
   |||
406 GGTGGGCT.....TATGTAAGTATATATATACAGACTTACTGCGTTGA 449
111 ....TTPSerProGlyLeuLeuLeuThrValSerSer 121
   |||
450 TGCGTGGGCGCAAGGACTCTGTGTCACCGTCCCTCA 486

seq_name: gb_om:OAVR21IG

seq_documentation_block:
LOCUS OAVR21IG 449 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(clone VR21).
ACCESSION 249166
VERSION 249166.1 GI:794107
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 449)
REFERENCE
AUTHORS Dufour V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, ILMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
2 (bases 1 to 449)
REFERENCE
AUTHORS Dufour V., Mallinck-S. and Nau F.
TITLE The sheep Ig variable region repertoire consists of a single VH
family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
FEATURES
source
1. .449 Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VR21"
/tissue_type="spleen"
/rearranged
39. .449
/gene="VH"
39. .>449
/gene="VH"
/codon_start=1
/product="VH region precursor"
/protein_id="CA89035.1"
/db_xref="GI:794108"
/translation="MNPMTPLFVL SAPRGVLSQVRLQSSPSLYKPSQTLSTCTVS
GSEITVSYGVNQAGKALEMIGIENQGCAGYHPLKSRSLSTITDTSKQVSLSS
SVTSEDTAMTYCVSRFFGKGTGPGGLTVSS"
39. .89
/gene="VH"
90. .449
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/product="VH region"
387. .449
D_segment

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BASP COUNT 93 a 138 c 123 g 95 t
ORIGIN
alignment_scores:
Quality: 443.50 Length: 121
Ratio: 4.069 Gaps: 2
Percent Similarity: 90.083 Percent Identity: 73.554

alignment_block:
US-09-786-015-2 x OAVR21IG ..
Align seg 1/1 to: OAVR21IG from: 1 to: 449

1 GluValGlnLeuGlnGlySerGlyProSerLeuValLysProSerGlnThr 17
|||||
96 CAGGTGGCGGTGCAGAGTGGGAGCCGCTGTGGAAGCCCTCACAGAC 145
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGlyV 34
|||||
146 COTGCCCTCACTGACAGGTCTCGGCTTCTCATTAACCACTACAGT 195
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGlnTyrLeuGly 50
|||||
196 TAGGCTGGGTCGCCAGGCTCCAGGAAAGCGCTGAGTGGCTGTGCT 245
51 ValSerSerGlyAlaLeuThrAlaTyrAspThrAlaLeuGlnSerArgLe 67
|||||
246 ATAGAAATGATGATGTGTCAGGCTATATCATCAGCCCTTAAGTCCCGCT 295
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||
296 CAGCATCAACAGGACACCTCCAGAGCCAGTCTCTCTGTCAGTGACCA 345
84 eValThrThrGluAspThrAlaLeuTyrTyrGlyAlaLeuSerValAsn 100
|||||
346 GCGTGACAAAGTGAGGACACGGCCACTACTGTGTGAGAAATTTTTC 395
101 GlyAspSerValProTyrGlyLeuAspTyrTTPSerProGlyLeuLeu 117
|||||
396 GGTGGAATATAC...TGGGGC.....TACTGGGCGCCAGGACTCTAGT 436
117 uThrValSerSer 121
|||||
437 CACGCTCTCTCA 449

seq_name: gb_om:AF172670

seq_documentation_block:
LOCUS AF172670 366 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 57 immunoglobulin heavy chain precursor (IGHV)
mRNA, partial cds.
ACCESSION AF172670
VERSION AF172670.1 GI:5815209
KEYWORDS
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 366)
REFERENCE
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL unpublished
REFERENCE
2 (bases 1 to 366)
White,G.P., Meusen,E.N.T. and Newton,S.E.
AUTHORS Direct Submission
TITLE Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,

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FEATURES             Melbourne, Victoria 3052, Australia
                        Location/Qualifiers
source               1..366
                        /organism="Ovis aries"
                        /db_xref="taxon:9940"
                        /clone="57"
                        /issue_type="abomasal lymph node"
                        /note="Isolated from animals infected with Haemonchus
                        contortus"
gene                 1..366
                        /gene="IGHV"
V_region             1..366
                        /gene="IGHV"
                        <1..>366
CDS                  /gene="IGHV"
                        /codon_start=1
                        /product="Immunoglobulin heavy chain precursor"
                        /protein_id="A052597.1"
                        /db_xref="GI:5815210"
                        /translation="QVQLQSGPSTLVKPSQTLSTCTVSGSLTYNAVGVRAQAPGKA
                        LEWVGAINSSGMDYNPALRSRLGIRDRSKNVSLSLSTVEDTAIVYYCYARHWIDN
                        TYGPATIDYWGSGELVTVSS"

BASE COUNT          87 a      107 c      96 g      76 t

ORIGIN
alignment_scores:
  Quality: 442.50      Length: 122
  Ratio: 4.060        Gaps: 1
  Percent Similarity: 89.344  Percent Identity: 72.131

alignment_block:
US-09-786-015-2 x AF172670 ..

Align seg 1/1 to: AF172670 from: 1 to: 366

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCACACTGCAGAGTGGGACCCGCTGGTGGAAGCCCTCACACAC 50
|||||
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCCTCACCTGCACGGCTCTGTGATTCATTACCAACTATGCTG 100
|||||
34 aLserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50
|||||
101 TAGCGTGGGTCGCCAGGCTCCAGGAAAGCATTTGGAGTGGGTGGTCC 150
|||||
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATATGGAGTACTGGGAAATACAGACTATTAACCCGCCCTGGAATCCGCACT 200
|||||
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
|||||
201 CGGATCATCACCGGAGACACTCCCAAGAACACAGGTCTCCCTGCTACAGACA 250
|||||
84 eValTrpThrGlnAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
251 GCGTCACACACTGCAGAGACCGCGGTACTACTGTGTAAAGACATTGGTAT 300
|||||
101 GlnAspSerVal...ProTyrGlyLeuAspTyrTrpSerProGlyLeu 116
|||||
301 GATATATCTTATGGACCGCATATATGACACTACGTGGGCCACAGCACTCT 350
|||||
116 uLeuThrValSerSer 121
|||||
351 GGTCAACGCTCTCTCA 366

seq_name: gb_om:AF172674
seq_documentation_block:
LOCUS AF172674 366 bp mRNA linear MAR 01-SEP-1999
DEFINITION Ovis aries clone 92 Immunoglobulin heavy chain precursor (IGHV)

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ACCESSION            mRNA, partial cds.
VERSION              AF172674
KEYWORDS              GI:5815217
SOURCE               AF172674.1
ORGANISM              Ovis aries
                        Sheep.
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                        Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                        Bovidae; Caprinae; Ovis.
REFERENCE             1 (bases 1 to 366)
AUTHORS              White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE                A single-chain variable region immunoglobulin library from the
                        abomasal lymph node of sheep infected with the gastrointestinal
                        nematode parasite Haemonchus contortus
JOURNAL              Unpublished
REFERENCE             2 (bases 1 to 366)
AUTHORS              White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE                Direct Submission
JOURNAL              Submitted (26-JUL-1999) School of Veterinary Science, The Center
                        for Animal Biotechnology, The University of Melbourne, Parkville,
                        Melbourne, Victoria 3052, Australia
FEATURES             Location/Qualifiers
source               1..366
                        /organism="Ovis aries"
                        /db_xref="taxon:9940"
                        /clone="92"
                        /issue_type="abomasal lymph node"
                        /note="Isolated from animals infected with Haemonchus
                        contortus"
gene                 1..366
                        /gene="IGHV"
V_region             1..366
                        /gene="IGHV"
                        <1..>366
CDS                  /gene="IGHV"
                        /codon_start=1
                        /product="Immunoglobulin heavy chain precursor"
                        /protein_id="A052601.1"
                        /db_xref="GI:5815218"
                        /translation="QVQLQSGPSTLVKPSQTLSTCTVSGFSLTYNAVHWVRAQPGKY
                        PEWLGSISGSGTYYNAALRSRLSITRDRSKSVSLSLSTVEDSNVYYCASDDIDG
                        VWDISYIHVYGPDLVTVSS"

BASE COUNT          80 a      111 c      97 g      78 t

ORIGIN
alignment_scores:
  Quality: 442.50      Length: 124
  Ratio: 4.097        Gaps: 3
  Percent Similarity: 87.097  Percent Identity: 75.000

alignment_block:
US-09-786-015-2 x AF172674 ..

Align seg 1/1 to: AF172674 from: 1 to: 366

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
1 CAGGTGCACACTGCAGAGTGGGACCCGCTGGTGGAAGCCCTCACACAC 50
|||||
17 rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCCTCACCTGCACGGCTCTGTGATTCATTACCAACTATGCTG 100
|||||
34 aLserTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50
|||||
101 TACACTGGGTCGCCAGGCTCCAGGAAAGTGGCCGAGTGGCTGTGAT 150
|||||
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 ATCAGCACTGTGGGAAGCACATATCATATGCGGCCCTGGAATCCGCACT 200
|||||
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84

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||||:|||||
201 CAGATCACGAGGACACCTCCAGAGCCAGTCCCTGCACGAGCC 250
84 erValThrGluSprThrAlaIleTyrTyrCysAlaLysSerValasn 100
|||||:|||||
251 GCGTACACAGGAGGAGCTGCGCGGTACTACTGTGCA...AGCGATAT 297
101 GlyAspSerVal.....ProTyrGlyLeuAspTyrTrpSerProgl 114
|||||:|||||
298 GGTGATGGTGTGTGCGATATATCCAT...ATCCACTACTGGGCCAGG 344
114 yLeuLeuThrValSerSer 121
|||||:|||||
345 ACTCGTGCACCGTCTCTCA 366

seq_name: gb_om:OAVRB15IG

seq documentation block:
LOCUS OAVRB15IG 456 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(cloze VRB15).
ACCESSION 249159.1 GI:794131
VERSION 249159.1
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 456)
Dufour,V.
REFERENCE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
2 (bases 1 to 456)
Dufour V., Malinge,S. and Nau,F.
AUTHORS The sheep Ig variable region repertoire consists of a single VH
TITLE family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
FEATURES
source
1..456
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VRB15"
/tissue="spleen"
/rearranged
37..456
/gene="VH"
37..>456
/gene="VH"
/codon_start=1
/product="VH region precursor"
/protein_id="CA89028.1"
/db_xref="GI:794132"
/translation="NMPITLFLVLSAPRCVLSQVLDGSGPELVPSQTLITCTVS
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37..87
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88..456
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/product="VH region"
385..456
/gene="VH"
/note="D-JH region"
BASE COUNT 100 a 138 c 112 g 106 t
ORIGIN
alignment_scores:
Quality: 442.00 Length: 121

Ratio: 4.131 Gaps: 0
Percent Similarity: 88.430 Percent Identity: 72.727
alignment block:
US-09-786-015-2 x OAVRB15IG ..
Align seq 1/1 to: OAVRB15IG from: 1 to: 456
1 glValGlnLeuGlnGluSerGlyProSerLeuValLysProSerGlnTh 17
|||||:|||||
94 CAGTTCACGCTTCAGAGGTCGCGACCCAGCTGTGGAACCTCACAAC 143
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||:|||||
144 CCTCTCTCTCACCTGCACGCTCTCGATTCATTAACACGATCTGCTG 193
34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGly 50
|||||:|||||
194 TAAAGTGGGTCCGCGAGGCTCCGGAAGGACGTGAGTGGGTGTAAAC 243
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||:|||||
244 ATTCATAATGATGGAATACATACATATATCCGCGCTGAAATCCGCGCT 293
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
|||||:|||||
294 CAGCATCTCCAGGAGGACCTCCAGAGCCAGTCTCTGCACAGCA 343
84 erValThrThrGluSprThrAlaIleTyrTyrCysAlaLysSerValasn 100
|||||:|||||
344 GCGTTACACTGAGGACAGGCGGTGTACTGTGCAAGGGGGGTATT 393
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProglLeuLeu 117
|||||:|||||
394 TATTACTCTACTGTGACTGTATCACTACACGAGGCCAGACTCTGTGT 443
117 uThrValSerSer 121
|||||:|||||
444 CACCGTCTCTCTCA 456

seq_name: gb_om:OAVR22IG

seq documentation block:
LOCUS OAVR22IG 434 bp mRNA linear MAM 04-FEB-1998
DEFINITION O.aries mRNA for immunoglobulin mu heavy chain variable region
(cloze VR22).
ACCESSION 249157.1 GI:899352
VERSION 249157.1
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 434)
Dufour,V.
REFERENCE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMIG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
2 (bases 1 to 434)
Dufour V., Malinge,S. and Nau,F.
AUTHORS The sheep Ig variable region repertoire consists of a single VH
TITLE family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
COMMENT On Jul 16, 1995 this sequence version replaced gi:794109.
FEATURES
source
1..434
Location/Qualifiers
/organism="Ovis aries"
/db_xref="taxon:9940"
/tissue="spleen"

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gene /rearranged  
39..434  
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CDS 39..>434  
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/db\_xref="GI:899353"  
/translation="NPPLMTLLFVLSAPRGVLSOVQLOESGFLVPSQTLSTCTVS  
GFLSRGVNWRQAPKSLSEWVGISWDSGTDYKPKLKSRLSTIRTSRSQVSLSL  
SVTSEDTAMYCAKSYFEMGPGLVTVSS"  
39..89  
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V\_region 90..434  
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/product="VH region"  
D\_segment 387..434  
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BASE COUNT 93 a 131 c 116 g 94 t  
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alignment\_scores:  
Quality: 441.00 Length: 121  
Ratio: 4.240 Gaps: 1  
Percent Similarity: 85.950 Percent Identity: 72.727  
alignment\_block:  
US-09-786-015-2 x OAVR22IG ..  
Align seg 1/1 to: OAVR22IG from: 1 to: 434  
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17  
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96 CAGGTGCAGCTGCAGAGTCGGACCCCTGCTGTGAAGCCCTCACAGAC 145  
|||||  
17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyGly 34  
|||||  
146 CCTCTCCCTCACCCTGCACGGTCTCTGGATTTCATTACCAAGCCGAGTG 195  
|||||  
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGlyGly 50  
|||||  
196 TTAACGTGGGTCCGCCAGGCTCCAGAAAGTCACTGGAGTGGTGGGCGC 245  
|||||  
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgle 67  
|||||  
246 ATATGGAGTGATGAGTACAGACTATTAACCGCGCCCTTGAATCCGACT 295  
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67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84  
|||||  
296 CACGATCACACAGGACACCTCCAGAGCCAAAGTCTCCTCTCAGTACGAC 345  
|||||  
84 erValThrThrGlnAspThrAlaIleTyrTyrcysAlaLysSerValAsn 100  
|||||  
346 GCGTGCACAGTGAGATACGGCATCTACTACTGTCACAAAGTAC... 392  
|||||  
101 GAlAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117  
|||||  
393 .....TTGAGTACTGGGGCCAGGACTCCTGGT 421  
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117 utrValSerSer 121  
:|||||  
422 CACGCTCTCCTCA 434  
seq\_name: gb\_om: BTU49778  
seq\_documentation\_block:  
LOCUS BTU49778 480 bp mRNA linear MAM 16-AUG-2001  
DEFINITION Bos taurus immunoglobulin rearranged heavy chain variable region  
ACCESSION U49778

VERSION U49778.1 GI:1293601  
KEYWORDS  
SOURCE  
ORGANISM BOS taurus  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.  
REFERENCE  
AUTHORS 1 (bases 1 to 480)  
TITLE Use of a single VH family and long CDR3s in the variable region of  
cattle Ig heavy chains  
JOURNAL Int. Immunol. 9 (1), 189-199 (1997)  
MEDLINE 97196871  
PUBMED 9043960  
REFERENCE  
AUTHORS 2 (bases 1 to 480)  
TITLE Berens,S.J., Wylie,D. and Lopez,O.J.  
Direct Submission  
JOURNAL Submitted (22-FEB-1996) Oswaldo J. Lopez, Biological Sciences,  
University of Nebraska, 325 Mantel Hall, Lincoln, NE 68588-0118,  
USA  
FEATURES  
source Location/Qualifiers  
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/protein\_id="AAA98659.1"  
/db\_xref="GI:1293602"  
/translation="NRINGVTVTLFVLSAPRGVLSOVQLOESGFLVPSQTLSTCTVS  
KPSQTLSTCTVSRSYSSYXSWTRKAPKRLLELGDLSGSGTGYNPKLKSRLST  
KNSKSOVSLSVTPEDTATYCAKDGVDYSGTGYTDYDAMGQGLVTVSS"  
CDS  
BASE COUNT 100 a 133 c 138 g 108 t 1 others  
ORIGIN  
alignment\_scores:  
Quality: 440.50 Length: 128  
Ratio: 4.117 Gaps: 1  
Percent Similarity: 83.594 Percent Identity: 70.312  
alignment\_block:  
US-09-786-015-2 x BTU49778 ..  
Align seg 1/1 to: BTU49778 from: 1 to: 480  
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97 CAGGTGCAGCTGCAGGAGTGGGGCCCAAGCTGTGAAGCCCTCACAGAC 146  
|||||  
17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyGly 34  
|||||  
147 CCTCTCCCTCACCCTGCATGCTCTGGATTCTCATGACGACGATATCTG 196  
|||||  
34 alserTPValArgGlnAlaProGlyLysAlaLeuGlnUtrPleuGlyGly 50  
|||||  
197 TTAAGTGGGTACCAAGGCTCCAGGAGGCGGTGGAGTGGTGGAT 246  
|||||  
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgle 67  
|||||  
247 ATTAAGCAGTGTGGAACACACAGCTATTAACCAAGCTTGAATCCGCGCT 296  
|||||  
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84  
|||||  
297 CACGATCACCAAGACCAACTCCAAAGACCAGTCTCTCTCAGTACGAC 346  
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84 erValThrThrGlnAspThrAlaIleTyrTyrcysAlaLysSerValAsn 100  
|||||  
347 GCGTGCACCTCAGGACACGGCCACATACATCTGTCGAAGATCGGGG 396  
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101 GLYASpSerValProTyrgly.....LeuAspTy 110
|||
397 GTGATATATAGTGTATGTTATGTTATGATACATACGTCATGC 446
110 rTTPSerProGlyLeuLeuLeuThrValSerSer 121
|||||
447 CTGGGGCAAGACTCCTGTCACCGCTCTCTCA 480

seq_name: gb_om:AF172659

seq_documentation_block:
LOCUS AF172659 351 bp mRNA linear MAM 01-SEP-1999
DEFINITION Ovis aries clone 1 immunoglobulin heavy chain precursor (IGHV)
mRNA, partial cds.
ACCESSION AF172659
VERSION AF172659.1 GI:5815187
KEYWORDS
SOURCE
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 351)
REFERENCE
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE A single-chain variable region immunoglobulin library from the
abomasal lymph node of sheep infected with the gastrointestinal
nematode parasite Haemonchus contortus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 351)
AUTHORS White,G.P., Meusen,E.N.T. and Newton,S.E.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1999) School of Veterinary Science, The Center
for Animal Biotechnology, The University of Melbourne, Parkville,
Melbourne, Victoria 3052, Australia
FEATURES
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1..351
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="1"
/tissue_type="abomasal lymph node"
/note="Isolated from animals infected with Haemonchus
contortus"
1..351
/gene="IGHV"
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/protein_id="AAD52586.1"
/db_xref="GI:5815188"
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PEWIGISGSGTYNPAKSKRTITRTDTSKQVSLSSVTSSEDTAVYYCADSLYVH
NTDYGPGILVTVSS"
BASE COUNT 79 a 109 c 95 g 68 t
ORIGIN
alignment_scores:
Quality: 440.00 Length: 121
Ratio: 4.151 Gaps: 1
Percent Similarity: 87.603 Percent Identity: 72.727

alignment_block:
US-09-786-015-2 x AF172659 ..
Align seg 1/1 to: AF172659 from: 1 to: 351
1 GtVaGlnLeuGInGInuSerGlyProSerLeuValLysProSerGInTh 17
|||||
1 CAGGTGCAACTGcAGcAGcTcGcGcACcCAGcCTGcTGAAGcCCcTcACAGAc 50

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17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrgly 34
|||||
51 CTTCTCCCTCGCTGCCTGACGCTCTCTGATTTCTCATTAACAGCAATAGTG 100
34 alSerTPValArgGlnAlaProGlyLysAlaLeuGlnTutPLeuGlygly 50
|||||
101 TAGGCTGGCTCCGCCAGCTCCAGGAAGGCTGCCGGCTGGTGGTGT 150
51 ValSerSerGlyValAlaLeuThrAlaTyAsnThrAlaLeuGlnSerTygLe 67
|||||
151 ATAGTAGAAGTGGGAGACCATATACCCGCGCTTGAAGTCCGCGCT 200
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||
201 CACCATCACCAGGAGACACCTCCAAGACCAAGCTCCTCCTCACTAGCA 250
84 eTyAlThrThrGluAspThrAlaLeuTyTrpCysAlaLysSerValAsn 100
|||||
251 CGGTGACAAAGTAGAGACGCGCTGTACTACTGTGcAGATAGTCTTC... 297
101 GLYASpSerValProTyrglyLeuAspTyTrpSerProGlyLeuLeu 117
|||||
298 .....TATGTCACAAATACCGACTACTGGGCGCCAGGACTCTGCT 338
117 urThrValSerSer 121
|||||
339 CACGCTCCTCTCA 351

seq_name: gb_om:OAVRA10IG
seq_documentation_block:
LOCUS OAVRA10IG 456 bp mRNA linear MAM 04-FEB-1998
DEFINITION O. aries mRNA for immunoglobulin mu heavy chain variable region
(clone VRA10).
ACCESSION Z49175.1 GI:794118
VERSION Z49175.1
KEYWORDS diversity region; immunoglobulin; immunoglobulin heavy chain;
joining region; variable region.
SOURCE
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
1 (bases 1 to 456)
REFERENCE
AUTHORS Dufour V.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1995) Dufour V., Faculte des Sciences, CNRS URA
1172, IBMTG, 40, avenue du Recteur Pineau, Poitiers, FRANCE, 86022
2 (bases 1 to 456)
AUTHORS Dufour V., Malinge,S. and Nau,F.
TITLE The sheep Ig variable region repertoire consists of a single VH
family
JOURNAL J. Immunol. 156 (6), 2163-2170 (1996)
MEDLINE 96310953
FEATURES
source location/Qualifiers
1..456
/organism="Ovis aries"
/db_xref="taxon:9940"
/clone="VRA10"
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/rearranged
37..456
/gene="VH"
37..>456
/gene="VH"
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/product="VH region precursor"
/protein_id="CAA89044.1"
/db_xref="GI:794119"
/translation="MNPLMTLLFVLSARGVLSVQVLESGPSLVKPSQITSLTCTVS
GFSLTSNNGVWVRAQAPKALEWVGDIVAGGSKESPAKPRILSTRDTSKQVSLSLSS
SVTETDRTAVYYCARDQPSGGVFGDYDYGPGILVTVSS"

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sig\_peptide 37.87 /gene="VH"  
V\_region 88.456 /gene="VH"  
D\_segment 385.456 /product="VH region"  
/gene="VH"  
/note="D-JH region"

BASE COUNT 100 a 136 c 125 g 95 t  
ORIGIN

alignment\_scores: Quality: 440.00 Length: 121  
Ratio: 4.151 Gaps: 0  
Percent Similarity: 87.603 Percent Identity: 71.901

alignment\_block:  
US-09-786-015-2 x OAVRA10IG ..

Align seg 1/1 to: OAVRA10IG from: 1 to: 456

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1 GlnValaInLeuGlnGlnSerGlyProSerLeuValIysProSerGlnTh 17
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94 CAGGTGCAGCTGAGGAGTGGGAGCCAGCCTGGTGAAGCCCTCAGAC 143
17 rLeuSerLeuThCysThrValSerGlyPheSerLeuThIysTyrGly 34
|||||
144 CTTCTCCCTCAGCTGACGGCTCTGTGATTCTCATTAACCAAGCAATATG 193
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
|||||
194 TAGGCTGGTCCGCGCAGGCTCCAGAAAGCAGCTGAGTGGTGTGAC 243
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||
244 ATATATGCTGTGGAGTAAGATAATATAGCCCGCCCTGAACCCCGGCT 293
67 uSerValThrArgAspThrSerIysSerGlnPheSerLeuSerLeuSers 84
|||||
294 CAGCATCACAGGAGACACTCCAGAGCCAGGTCTCCCTGTCACTGAGCA 343
84 erValThrThrGluAspThrAlaIleTyrTyrCysAlaIysSerValAsn 100
|||||
344 GCGTGAACAACGAGACACGCGCTGACTACTGTCCAGAGATCAGCCT 393
101 GLyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
|||||
394 AGTAGTGGCGTGTGGTATTACGACTACTGCGGCGCCAGGACTACTGTGT 443
117 uThrValSerSer 121
|||||
444 CACGCTCTCTCA 456
```

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17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
51 CCTCTCCCTACCTGCACGGCTCTGTGATTCCTATTACCAAGATATGCTG 100
34 a1SerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
|||||
101 TTAGTTGGGTCCGCGAGCTCCAGAAAGGCGCTTGAGTGGTGGT 150
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
151 GTCTCCAGTGTGCTCACTAACAGCCTATTAACACAGCCCTACAGTCCGACT 200
67 uSerValThrArgAspThrSerIleSerGlnPheSerLeuSerLeuSers 84
|||||
201 CACGCTCACCGAGGACACCTCCAAAGAGCCAAATTCCTCCCTGACTGAGCA 250
84 eValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
251 GCGTGACTACTGAGACACGGCCATTACTACTGTGCGAAATCTGTCAT 300
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
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301 GGTGACAGTGTCTCTATGTTGACTGACTGAGCCGACGACTCCTACT 350
117 uThrValSerSer 121
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351 CACCGTCTCCTCA 363

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH76441

seq_documentation_block:
ID AAH76441 standard; cDNA; 460 BP.
XX
AC AAH76441;
XX
XX 22-OCT-2001 (first entry)
XX
DE Humanised anti-CTLA4 heavy chain cDNA.
XX
XX Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KM immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KM T cell; humanised antibody; autoimmune disorder; graft rejection;
KM allergy; heavy chain; ss.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH CDS 12..437
FT /*tag= a
FT /product= "humanised anti-CTLA4 heavy chain"
XX
XX WO200154732-A1.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-US02653.
XX
XX 27-JAN-2000; 2000US-0178473.
XX
XX (GENY ) GENETICS INST INC.
XX
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI O'Hara D, Hinton P, Tsurushita N;
XX
XX MPI: 2001-483195/52.
XX
XX P-PSDB; AAG66523.
XX
XX Novel antibody-toxic group conjugate comprising an antibody that
PT recognizes a molecule expressed only on activated T cells; useful for
PT modulating immune response for treating autoimmune disorder; allergic
PT response
```

```
XX
PS Example 7; Page 118; 123p; English.
XX
CC The invention relates to an antibody-toxic group conjugate comprising
CC an antibody that specifically recognises a molecule expressed only on
CC activated T cells, and a toxic group. The T cell molecule is
CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
CC The antibody of the invention is a humanised anti-CTLA4 antibody
CC comprising a sequence of 128 or 142 amino acids fully defined in the
CC specification. The antibody-toxic group conjugate is useful for
CC modulating the immune response in a subject suffering from a disorder
CC or condition such as autoimmune disorder, immune response to a graft,
CC allergic response or an immune response to a therapeutic protein.
CC The antibody is also useful for research purposes, e.g., in staining
CC and isolating CTLA4-bearing cells. The antibody is also useful for
CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
CC fragments of the receptor, for vaccine preparation, and for determining
CC the effectiveness of an agent to down-regulate CTLA4 activity. The
CC present sequence encodes the heavy chain of humanised anti-CTLA4
CC antibody.
XX
SQ Sequence 460 BP; 107 A; 124 C; 116 G; 113 T; 0 other;

alignment_scores:
Quality: 417.00 Length: 123
Ratio: 3.971 Gaps: 1
Percent Similarity: 85.366 Percent Identity: 66.667

alignment_block:
US-09-786-015-2 x AAH76441 ..

Align seg 1/1 to: AAH76441 from: 1 to: 460

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69 CAGGTGACGCTGCACAGAGTCAGACCTGGCTGTGAGACCTCACAGAC 118
17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
119 ACCTGCTTACCTGACCTGCTCTGTGGTTTCATTATCACTCATATGCTG 168
34 a1SerTrpValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
|||||
169 TATATTGGGTTCGCCACGCTCCAGAAAGGCTGCGAGTGGCGAGTA 218
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
|||||
219 ATATGGCTGTGTGTACCAACAATTAATTCGCTCTCATGTCCAGACT 268
67 uSerValThrArgAspThrSerIleSerGlnPheSerLeuSerLeuSers 84
|||||
269 GACAAATCAGCAAGACACATCCAAAGAACCAAGTTCTCTTAACCTGACA 318
84 eValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
|||||
319 GTGTGACTGACGCGGACACCGCTTACTACTGTGCGCAGGCCGCCG 368
101 GlyAspSerValPro.....TyrGlyLeuAspTyrTrpSerProGlyLe 115
|||||
369 CACGCTATGATGAAGAGAGGCTATGACTACTACTGCGGACAGGAC 418
115 uLeuLeuThrValSerSer 121
|||||
419 CCTAGTCACAGTCTCCTCA 437

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH76443

seq_documentation_block:
ID AAH76443 standard; cDNA; 468 BP.
XX
XX AAH76443;
XX
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XX	22-OCT-2001	(first entry)
DE	Humanised anti-CTLA4 heavy chain cDNA.	
KW	Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4; immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;	
KW	T cell; humanised antibody; autoimmune disorder; graft rejection;	
KW	allergy; heavy chain; ss.	
OS	Homo sapiens.	
OS	Mus musculus.	
XX	Synthetic.	
FT	Key	
FT	Location/Qualifiers	
FT	16..441	
FT	/tag=a	
FT	/product="humanised anti-CTLA4 heavy chain"	
XX	WO200154732-A1.	
PD	02-AUG-2001.	
XX	26-JAN-2001; 2001WO-US02653.	
XX	27-JAN-2000; 2000US-0178473.	
PA	(GEMV ) GENETICS INST INC.	
XX	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;	
PI	O'Hara D, Hinton P, Tsurushita N;	
XX	WPI: 2001-483195/52.	
DR	P-PSDB: AAG65523.	
PT	Novel antibody-toxic group conjugate comprising an antibody that	
PT	recognizes a molecule expressed only on activated T cells, useful for	
PT	modulating immune response for treating autoimmune disorder, allergic	
PT	response	
PS	Example 7; Fig 10; 123pp; English.	
XX	The invention relates to an antibody-toxic group conjugate comprising	
CC	an antibody that specifically recognises a molecule expressed only on	
CC	activated T cells, and a toxic group. The T cell molecule is	
CC	preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).	
CC	The antibody of the invention is a humanised anti-CTLA4 antibody	
CC	comprising a sequence of 128 or 142 amino acids fully defined in the	
CC	specification. The antibody-toxic group conjugate is useful for	
CC	modulating the immune response in a subject suffering from a disorder	
CC	or condition such as autoimmune disorder, immune response to a graft,	
CC	allergic response or an immune response to a therapeutic protein.	
CC	The antibody is also useful for research purposes, e.g., in staining	
CC	and isolating CTLA4-bearing cells. The antibody is also useful for	
CC	T-cell typing, for isolating specific II-2 receptor-bearing cells or	
CC	fragments of the receptor, for vaccine preparation, and for determining	
CC	the effectiveness of an agent to down-regulate CTLA4 activity. The	
CC	present sequence encodes the heavy chain of humanised anti-CTLA4	
XX	antibody.	
XX	Sequence 468 BP; 111 A; 124 C; 116 G; 117 T; 0 other;	

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alignment_scores:
  Quality: 417.00
  Ratio: 3.971
  Percent Similarity: 85.366
  Length: 123
  Gaps: 1
  Percent Identity: 66.667
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alignment_block:
US-09-786-015-2 x AAH76443 .
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Align seg 1/1 to: AAH76443 from: 1 to: 4688

1 GlnValGlnLeuGlnGlnIuserGlyProSerLeuValLysProSerGlnTh 17

[illegible]

seq\_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: AAT90980

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seq_documentation_block:
ID   AAT90980 standard; DNA; 411 BP.
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AC AAT90980;

DT 07-JUL-1998 (first entry)

Nucleotide sequence of the heavy chain of HUM4TS.22.

KM Hm4T5.22; antibody; platelet derived growth beta receptor; PDGF-R beta  
KM inhibition; intimal hyperplasia; restenosis; angioplasty;  
KM heavy chain; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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100	100	100

FT	product=	"Heavy chain of MATS.22"
FT	.mat_peptide	58..411

PN WO9737029-A1.

PD 09-OCT-1997.

PF 19-MAR-1997; 97WO-US04198.

PR 22-MAR-1996; 96US-0621751.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Chang CN, Landolfi NF, Martin U;

DR WPI; 1997-503114/46.

DR P-PSDB; AAW30273.

PT Antibodies to platelet derived growth factor beta receptor - Inhibit  
PDGF BB-induced proliferation of cells expressing the receptor, used

PT particularly for inhibiting intimal hyperplasia  
 XX  
 XX Example 5; Fig 2C; 87pp; English.  
 XX  
 CC This is the nucleotide sequence for the heavy chain of Hum47S.22, a  
 CC novel antibody which specifically binds to the platelet derived  
 CC growth beta receptor (PDGF-R beta), but not within the fifth  
 CC extracellular Ig-like domain, where the antibody inhibits PDGF  
 CC BB-induced proliferation of a cell expressing the PDGF beta receptor.  
 CC The antibody can be used in a method of inhibiting intimal hyperplasia  
 CC in the vasculature of a mammal. The antibodies can be used for the  
 CC treatment of disorders related to PDGF activity such as disorders  
 CC involving proliferation of smooth muscle cells, and including  
 CC restenosis following angioplasty.  
 CC  
 XX  
 SQ Sequence 411 BP; 85 A; 115 C; 112 G; 99 T; 0 other;  
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 Quality: 409.50 Length: 121  
 Ratio: 3.863 Gaps: 1  
 Percent Similarity: 87.603 Percent Identity: 65.289  
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 58 CAGGTGCGAGCTGCGAGAGTGGGCCAGGAGTGGTGAAGCCTGGAGAC 107  
 |||||  
 17 rleuSerleuthrCysThrValSerGlyPheserleuthrIstYrGlyV 34  
 |||||  
 108 CCTGTCCTCACTGACCTGCTCTGCTTCTCTTACCACTATGCTA 157  
 |||||  
 34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50  
 |||||  
 158 TAAACTGGGTTGCGGACGACGAGGAGGAGTGGAGTGGGATG 207  
 |||||  
 51 ValSerSerGlyAlaLeuThrAlaTrpAsnThrAlaLeuGlnSerArgLe 67  
 |||||  
 208 ATATGAGTGGTGGAGGACCAAGTATATCTGCTCTCAATCCGACT 257  
 |||||  
 67 uSerValThrArgAspThrSerLysSerGlnPheserleuSerLeuSers 84  
 |||||  
 258 GACCTATATCAAAAGACACTTCACAGACAGGTTCCCTGAAGCTGAGCT 307  
 |||||  
 84 erValThrThrGlnAspThrAlaLeuTrpYrCysAlaLysSerValAsn 100  
 |||||  
 308 CTGTTACCGCTGGGACAGCGGCGCTGTATTACTGTGCGAGACT..... 351  
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 101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeuLe 117  
 |||||  
 352 ...GGGAGGAGGGGATATTCTTCTTACCTACTGAGGCGCAGGGAACCTGGT 398  
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 117 uThrValSerSer 121  
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 399 CACCGTCTCTCA 411  
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 seq\_documentation\_block:  
 ID AAQ11847 standard; DNA: 363 BP.  
 XX  
 AC AAQ11847;  
 XX  
 DT 31-JUL-1991 (first entry)  
 XX  
 DE Human anti-Placental alkaline phosphatase VH gene.  
 XX  
 KM Placental alkaline phosphatase; antibody; cancer; heavy chain;  
 KM PLAP; CDR; SS.

XX Homo sapiens.  
 OS  
 XX  
 FH Key  
 FT misc\_feature  
 FT 91.105  
 FT /tag= a  
 FT /label= CDR1  
 FT 148.195  
 FT /tag= b  
 FT /label= CDR2  
 FT 292.330  
 FT /tag= c  
 FT /label= CDR3  
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 XX EP429242-A.  
 PN  
 XX  
 PD 29-MAY-1991.  
 XX  
 XX 14-NOV-1990; 90EP-0312407.  
 PF  
 XX 07-SEP-1990; 90GB-0019552.  
 PR  
 XX 17-NOV-1989; 89GB-0026045.  
 XX  
 PA (UNIL ) UNILEVER PLC.  
 XX  
 XX Verhoeven ME;  
 PI  
 XX WPI: 1991-157662/22.  
 DR  
 XX P-PSDB: AAR11986.  
 XX  
 PT Synthetic specific binder for human placental alkaline  
 PT phosphatase - for treating and diagnosing cancers e.g. breast,  
 PT ovarian and colon cancers and pleural effusions  
 XX  
 PS Disclosure: Fig 10; 28pp; English.  
 XX  
 CC The murine anti-PLAP VH gene (AAQ11845) contains 3 CDRs which are used  
 CC to reshape the human anti-PLAP VH gene. The murine anti-PLAP Vh gene  
 CC (AAQ11846) CDRs were used to reshape the human anti-PLAP gene Vh  
 CC (AAQ11848). The specific binder for human PLAP contains at least  
 CC one of the former 3 CDRs and/or at least one of the latter CDRs.  
 CC The produced antibodies are more readily tolerated when administered  
 CC to a human patient. Antibody reagents can be used to identify, e.g.  
 CC by serum testing or imaging, and/or to treat PLAP-producing cancers.  
 CC Such cancers can occur as, e.g. breast cancer, ovarian cancer and  
 CC colon cancer or can manifest themselves as liquids such as pleural  
 CC effusions.  
 CC  
 SQ Sequence 363 BP; 88 A; 98 C; 103 G; 74 T; 0 other;  
 alignment\_scores:  
 Quality: 391.00 Length: 121  
 Ratio: 3.833 Gaps: 0  
 Percent Similarity: 84.298 Percent Identity: 62.810  
 alignment\_block:  
 US-09-786-015-2 x AAQ11847 ..  
 Align seg 1/1 to: AAQ11847 from: 1 to: 363  
 1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17  
 |||||  
 1 CAGTCCAACTGCAAGAGAGCGGCTGCTGAGACCTAGCCAGAC 50  
 |||||  
 17 rleuSerleuthrCysThrValSerGlyPheserleuthrIstYrGlyV 34  
 |||||  
 51 CCTGAGCCTGAGCTGACCGCTGCTGCTCACTTCACTGATGATGCGCTG 100  
 |||||  
 34 alSerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGly 50  
 |||||  
 101 TAACTGGTGGAGACAGCCACTGAGCAGAGCTTGTGATGATGCGCTA 150



```

51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
151 ATATGGAGACGGGACACAAATATCATTCACCTCTCATATCCAGAGT 200
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSerS 84
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
201 GACAAATGCTGCTAGACACAGCAAGAACAGGTCAGCTGAGCTAGACGA 250
84 eValThrThrGluAspThrAlaLeuTyrTyrCysAlaLysSerValAsn 100
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
251 GCGGACAGACCGCGCACCGGCTATATATGTCGAAGACCCCACTAC 300
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
301 GGTAGCAGCTACCTGCGGCTATGATGATCTGGGCTCAAGCCACCTCGT 350
117 uThrValSerSer 121
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
351 CACAGTCTCCTCA 363

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seq\_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AA186310

seq\_documentation\_block:  
ID AAT86310 standard; DNA; 714 BP.

AC AAT86310;

DT 06-APR-1998 (first entry)

DE Single chain anti-disialoganglioside GD2 antibody 3G6-scfv.

XX Antibody construct: disialoganglioside; GD2; single chain Fv fragment;

KM scfv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;

KM tissue imaging; target delivery; toxin; streptavidin;

KM pro-drug converting enzyme; GD2-targeted lymphocyte; ss.

XX Synthetic.

XX WO9734634-A1.

XX 25-SEP-1997.

XX 20-MAR-1997; 97WO-US04427.

XX PR 20-MAR-1996; 96US-0013703.

XX PA (SLOAN ) SLOAN KETTERING INST CANCER RES.

XX Cheung NV, Guo H, Larson SM, Rivlin K, Sadelain M;

XX WPI: 1997-479996/44.

XX Recombinant single chain anti-disialoganglioside GD2 antibody -

XX useful to detect tumour cells expressing GD2 and to target

XX therapeutic agents, e.g. toxins, to such cells

XX Disclosure: Page 11-12; 31pp; English.

XX The present sequence encodes a recombinant single chain peptide,

XX 3G6-scfv. The peptide is an antibody construct comprising the variable

XX regions of the heavy and light chains of an antibody against

XX disialoganglioside (GD2) as a single chain Fv fragment (scfv). GD2 occurs

XX in many tumours types including neuroblastoma, osteosarcoma and other

XX soft tissue sarcomas, medulloblastomas, high grade astrocytomas,

XX melanomas and small cell lung cancer. The peptide can be detectably

XX labelled, preferably with 99m-Tc, for tissue imaging of cells expressing

XX GD2. It can also be used to target delivery of a therapeutic or

XX pre-therapeutic agent, such as a toxin, streptavidin or a pro-drug

XX converting enzyme, to cells expressing GD2. The peptide may further

XX comprise GD8 to facilitate the formation of GD2-targeted lymphocytes.

XX T cells containing the peptide can also be used to target GD2-producing

XX tumour cells.

Sequence 714 BP; 174 A; 168 C; 205 G; 167 T; 0 other;

alignment\_scores: Quality: 391.00 Length: 121

Percent Similarity: 85.124 Ratio: 3.796 Gaps: 1

Percent Identity: 61.983

alignment\_block: US-09-786-015-2 x AAT86310 ..

Align seg 1/1 to: AAT86310 from: 1 to: 714

```

1 GlnValGlnLeuGlnGlnSerGlyProSerLeuVallyProSerGlnTh 17
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
358 CAGGTGCGAGGTGAAGAGTCAAGACCTGCGCTGCGCGCCCTCACACAG 407
17 rLeuSerLeuThrCysThrValSerGlyPheSerLeuThrIlyTyrGly 34
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
408 CCTGTCATCATCTGCACTGCTCTGCTGCTTTTCATTAACCAATTAAGTG 457
34 aISerTPValArgGlnAlaProGlyLysAlaLeuGluTrpLeuGlyGly 50
   || ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
458 TACACTGGGTTGCGCCAGCCTCCAGGAAAGGCTGAGTGGCTGGAGTA 507
51 ValSerSerGlyAlaLeuThrAlaTyrAspThrAlaLeuGlnSerArgLe 67
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
508 ATATGGGCTGTGGAGACACAAATATATATGCGCTCTTAATGTCAGACT 557
67 uSerValThrArgAspThrSerIlySerGlnPheSerLeuSerLeuSerS 84
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
558 GAGCATGACGACAGGACACCTCCAGACCAAGTTTCTTAATAATGACAA 607
84 eValThrThrGlnAspThrAlaLeuTyrTyrCysAlaLysSerValAsn 100
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
608 GTCGTCAAACTGATGACACAGCATGACTACTGTGCGAGT.....CGG 651
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
   ||||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
652 GGGGTTACTACGCGCTATGCTTTGGACTACTGCGGTCAAGCAACCTCAGT 701
117 uThrValSerSer 121
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
702 CACCGTCTCCTCA 714

```

seq\_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AA186312

seq\_documentation\_block:

ID AAT86312 standard; DNA; 1173 BP.

AC AAT86312;

DT 06-APR-1998 (first entry)

DE Single chain anti-disialoganglioside GD2 antibody 3G6-scfv-streptavidin.

KM Antibody construct: disialoganglioside; GD2; single chain Fv fragment;

KM scfv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;

KM tissue imaging; target delivery; toxin; streptavidin;

KM pro-drug converting enzyme; GD2-targeted lymphocyte; ss.

XX Synthetic.

XX Key location/Qualifiers

FT misc\_feature 1..714

FT misc\_feature /tag- a

FT misc\_feature /note- "encodes single chain Fv fragment of

FT misc\_feature /tag- b

FT misc\_feature /note- "linker sequence"

FT misc\_feature 739..0

FT misc\_feature /tag- c



alignment\_scores:                      Quality: 390.50                      Length: 121  
    Ratio: 3.828                      Gaps: 1  
Percent Similarity: 84.298              Percent Identity: 61.983

alignment\_block:  
US-09-786-015-2 x AAT77852 ..

Align seg 1/1 to: AAT77852 from: 1 to: 420

```
1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61  CAGGTGCAGTCAAGAGAGTCAAGAGCCTGGCGCTGCGCCCTCACAGAG 110
17  rleuSerLeuThrCysThrValSerGlyPheSerLeuThyLysGly 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
111 CCGTGCATCACTTCGACTGCTCTGGGTTTTCATTAACTGCTATGCTG 160
34  aSerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
161 TACACTGGGTGGCCAGCCTCCAGGAAGGGTCTGGAGTGGCGGAGTA 210
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArg 67
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
211 ATATGGGCTGGTGGAGCATTAATTAATTCGGCTCTCATGTCAGACT 260
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261 GAGCATCAGCAAGACACTTCACAGAGCCAGATTTCCTTAATAATGAGCA 310
84  eValThrThrGlnAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
   ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
311 GCTGCAACTGATGACAGACAGCATGACTGACTGTCAGAGCCTAT... 357
101  GlysAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
358 GGGACTACGACTGACATGCTATGACTACTGGGTCACAGAACCTCAGT 407
117  uThrValSerSer 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
408 CACCGCTCTCTCA 420
```

seq\_name: /SIDSI/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA38902

seq\_documentation\_block:

ID AAA38902 standard; DNA: 357 BP.

```
XX  AAA38902;
AC  29-AUG-2000 (first entry)
DT  260F9 hybridoma VH domain encoding DNA SEQ ID NO:13.
DE  Antigen binding site: immunoglobulin; cancer antigen; immunological;
XX  antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
XX  specific binding assay; affinity purification; drug targeting;
XX  toxin targeting; imaging; genetic; therapeutic; ss.
OS  Homo sapiens.
PN  US6054561-A.
XX  25-APR-2000.
PD  07-JUN-1995; 95US-0483749.
XX  21-MAR-1986; 86US-0842476.
PR  08-MAY-1988; 88US-0190778.
PR  08-FEB-1984; 84US-0577976.
PR  11-JAN-1985; 85US-0690750.
PR  11-AUG-1994; 94US-0288981.
XX  (CHIR ) CHIRON CORP.
PA
```

XX Ring DB:  
PI WPI: 2000-338508/29.  
XX P-PSDB: AAY90818.  
DR Monoclonal antibody capable of binding to human breast cancer antigen  
PT useful for affinity purification, drug or toxin targeting, imaging, and  
PT treating cancer

XX Disclosure; Fig 7; 57pp; English.

XX The present invention describes a monoclonal antibody (Mab) (I) that  
XX binds to a human breast cancer antigen that is also bound by Mab 454C11  
XX and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also  
XX described is a hybridoma that produces (I). (I) is useful in specific  
XX binding assays, affinity purification, drug or toxin targeting, imaging,  
XX and genetic or immunological therapeutics for various cancers. The  
XX present sequence encodes a VH domain derived from a 260F9 hybridoma,  
XX which is used in the exemplification of the present invention.

SQ Sequence 357 BP; 89 A; 89 C; 93 G; 86 T; 0 other:

alignment\_scores:                      Quality: 389.00                      Length: 121  
    Ratio: 3.814                      Gaps: 1  
Percent Similarity: 84.298              Percent Identity: 61.983

alignment\_block:  
US-09-786-015-2 x AAA38902 ..

Align seg 1/1 to: AAA38902 from: 1 to: 357

```
1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1  GAGGTGCAGTCAAGAGAGTCAAGAGCCTGGCGCTGCGCCCTCACAGAG 50
17  rleuSerLeuThrCysThrValSerGlyPheSerLeuThyLysGly 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51  GCTGTCATCACTTCGCTGCTCTGGGTTTTCATTAACTGCTATGCTG 100
34  aSerTrpValArgGlnAlaProGlyLysAlaLeuGlnTrpLeuGlyGly 50
   || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
101 TACACTGGGTGGCCAGCCTCCAGGAAGGGTCTGAGTGGCGGAGCA 150
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArg 67
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
151 ATATGGGCTGGTGGAGCATTAATTAATTCGGCTCTCATGTCAGACT 200
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLys 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
201 GAGCATCAGCAAGACACTTCACAGAGCCAGATTTCCTTAATAATGAGCA 250
84  eValThrThrGlnAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
   ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
251 TCTGCAAACTGATGACACAGCATGACTGACTGCTGCCAGA....GAC 294
101  GlysAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
295 GGGGATTACGACTCTTATCTTGGACTGAGTGGGTCAGAGAACCTCAGT 344
117  uThrValSerSer 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
345 CACCGTCTCTCA 357
```

seq\_name: /SIDSI/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA08033

seq\_documentation\_block:

ID AAA08033 standard; DNA: 840 BP.

```
XX  AAA08033;
AC
XX
```

DT	19-JUN-2000	(first entry)
XX	Antibody fragment scFv Tg8-D4 polynucleotide sequence SEQ ID NO:1.	
DE		
XX		
KW	Glutenin subunit; wheat; antibody; immunoassay; identification;	
KW	plant breeding; grain; flour; bread; pasta; ds.	
XX		
OS	Mus musculus.	
XX		
PN	WO200012557-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	27-AUG-1999;	99WO-AU00690.
XX		
PR	28-AUG-1998;	98AU-0005548.
XX		
PA	(QUAL-) QUALITY WHEAT CRC LTD.	
XX		
PI	Giersch TM, Skerittt JH, Hill AS;	
XX		
DR	WPI: 2000-256593/22.	

PT neuroblastoma and glioma.  
XX  
PS Disclosure: Page 109; 191pp; English.  
XX  
CC Chimeric human Ab expression vectors are constructed by inserting  
CC the Ab heavy and light chain variable region-encoding CDNA  
CC isolated from hybridomas producing a mouse or rat monoclonal Ab  
CC reacting with the ganglioside GM2 respectively into an expression  
CC vector for use in animal cells which contains the human Ab heavy and  
CC light chain constant region-encoding CDNA. The expression vectors  
CC are introduced into animal cells and the transformant thus obtained  
CC is cultured for the prodn. of a chimeric human Ab reacting with the  
CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric  
CC human Abs will not cause anti-mouse Ig Ab prodn. In the patient's  
CC body but show a prolonged blood half-life, with a reduced frequency  
CC of adverse effects, so that it can be expected to be superior  
CC to mouse monoclonal Abs in the efficacy in the treatment of human  
CC cancer, for instance.  
CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603  
CC heavy and light chain sequences are given in AA045426-30.  
CC CDR regions for use in chimeric Abs are indicated in the  
CC Features Table.  
XX  
SQ Sequence 405 BP; 95 A; 110 C; 103 G; 97 T; 0 other;

alignment\_scores:  
Quality: 388.50 Length: 121  
Ratio: 3.809 Gaps: 1  
Percent Similarity: 84.298 Percent Identity: 62.810

alignment\_block:  
US-09-786-015-2 x AA045429 ..

Align seg 1/1 to: AA045429 from: 1 to: 405

```
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
67 CAAGTCAGCTGAAGAGGAGCAGCTGCTGCTGTCAGCGCCCTCAGAC 116
17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
117 CCGTCCCTCACCCTGCACCTGCTCTGCGGTCTCATTAACACGCTATCTG 166
34 aIsertPValAfcGlnAlaProGlyLysAlaLeuGlnUTPleuGlyGly 50
|||||
167 TAAGCTGGGTTCCGACCTCCAGAGAAAGGCTGGAGTGAGATTGACACA 216
51 ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgle 67
|||||
217 ATATCAAGCTGTGAAGCACATATTAATTCAGCTCTCAATCAGCACT 266
67 uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSers 84
|||||
267 GACACATCAGCAGGAGACACCTCAAGACCAAGTTTCTTAAATAATGAACA 316
84 eValAlaGlnLeuGlnAlaIleTyrGlyCysAlaLysSerValAsn 100
|||||
317 GTCTGCAACTGAAGACACACCATGACTTCTGTGCCCCCTTCGAGGGG 366
101 GlyAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
|||||
367 GCC.....TGGGGCCCAAGAGATCATGCT 389
117 uThrValSerSer 121
|||||
390 CACAGCTCTCCTCA 402
```

seq\_name: /sids1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAx9477

seq\_documentation\_block:

ID AAX9477 standard; CDNA to mRNA; 405 BP.  
XX

AC AAX9477;  
XX  
XX 04-NOV-1999 (first entry)  
XX  
XX Antibody heavy chain KM-603.  
DE  
XX antibody; nucleotide; genomic; hypervariable region;  
KW chimeric; light chain; heavy chain; ds.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 10..405 /\*tag= a  
FT FT /product= "Rat anti-GM2 heavy chain"  
FT sig\_peptide 10..66 /\*tag= b  
FT mat\_peptide 67..405 /\*tag= c  
XX  
XX US5939532-A.  
XX  
XX 17-AUG-1999.  
XX  
XX 07-JUN-1995; 95US-0483528.  
XX  
XX 07-JUN-1995; 95US-0483528.  
XX  
XX 07-SEP-1993; 93US-0116778.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Hanai N, Hasegawa M, Kolke M, Kuvana Y, Nakamura K;  
XX Shitara K;  
XX  
XX WPI, 1999-468416/39.  
XX  
XX P-PSDB; AAY28359.

Chimeric human antibody expression vectors

Example 1; Column 87-89; 188pp; English.

This antibody chain is derived from Hybridoma cells producing the Rat  
CC Anti-GM2 Monoclonal Antibody KM-603.  
CC The chimeric human antibodies are useful in the treatment of  
CC cancer, especially that which is of neural ectodermal origin.  
CC In contrast to prior art constructs based on mouse monoclonal  
CC antibodies, the chimeric human antibodies do not cause anti-mouse  
CC immunoglobulin production.  
CC The chimeric human antibodies have a prolonged half-life and a reduced  
CC frequency of adverse effects when compared to mouse monoclonal  
CC antibodies.  
XX  
XX

Sequence 405 BP; 95 A; 110 C; 103 G; 97 T; 0 other;

alignment\_scores:  
Quality: 388.50 Length: 121  
Ratio: 3.809 Gaps: 1  
Percent Similarity: 84.298 Percent Identity: 62.810

alignment\_block:  
US-09-786-015-2 x AAX9477 ..

Align seg 1/1 to: AAX9477 from: 1 to: 405

```
1 GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
|||||
67 CAAGTCAGCTGAAGAGGAGCAGCTGCTGCTGTCAGCGCCCTCAGAC 116
17 rleuSerLeuThrCysThrValSerGlyPheSerLeuThrLysTyrGly 34
|||||
117 CCGTCCCTCACCCTGCACCTGCTCTGCGGTCTCATTAACACGCTATCTG 166
```

```

34  alserTPValArgGlnAlaProGlyLysAlaLeuGlnTTPLeuGlyGly 50
    |||
167  TAACTGGTGGTGGCCAGCTCCAGGAAGGCTCGAGTGGATTGCAGCA 216
    |||
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
    |||
217  ATATCAAGTGTGGAGCAGCATATTATTAATTCAGCTCTCAATCAGACT 266
    |||
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
    |||
267  GAGCATCAGACAGGAGCAGCTCCAGACCAAGTTCTCTTAATAATGACAA 316
    |||
84  erValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
    |||
317  CTCGCAAACTGGAAGACACAGCCATGACTCTCTGCCCCCTTCGAGGG 366
    |||
101  GLYAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
    |||
367  GCC.....TGGGGCCAGGAGTCATGCT 389
    |||
117  uThrValSerSer 121
    |||
390  CACAGTCTCCTCA 402
    |||

```

seq\_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ13110

seq\_documentation\_block:

ID AAQ13110 standard; DNA; 407 BP.

XX AAQ13110;

DT 21-OCT-1991 (first entry)

XX HuVhlys.

XX Hypervariable region; light chain; heavy chain; CDR; RBS; antigen; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 10..369

FT /tag= a

FT /label= HuVhlys

FT misc\_RNA 112..126

FT /tag= b

FT /label= CDR1

FT misc\_RNA 169..216

FT /tag= c

FT /label= CDR2

FT misc\_RNA 311..336

FT /tag= d

FT /label= CDR3

XX EP440146-A.

PN EP440147-A.

XX 07-AUG-1991.

PD 28-JAN-1991.

PF 91BP-0101094.

XX 09-FEB-1990.

PR 90DE-4003880.

PR 01-FEB-1990.

XX 90DE-4002897.

XX (BEHW ) BEHRINGER AG.

XX Little M, Bretling FB, Seehaus T, Dubel S, Kiewinghaus I;

PI WPI: 1991-231878/32.

XX Synthetic human antibody library - produced by expression of DNA

PT confg. random sequences for hyper-variable regions

XX Disclosure; Page 10; 14pp; German.

```

XX Synthetic human antibody libraries can be produced by using
CC randomly synthesised oligonucleotides coding for each of the three
CC hypervariable regions in the variable parts of the heavy and light
CC chains (regions CDR1, CDR2 and CDR3). Two batches of oligonucleotides
CC are used for the synthesis of the variable domains. These are
CC ligated and inserted into expression vector pFMT.
CC pFMT (EP-440147) comprises a modified pRR233-2 plasmid (SalI-BamHI
CC deleted, HindIII replaced by BamHI) with an insert comprising a
CC first leader sequence (PL) (AAQ13098) from a bacterial peptidase
CC gene, a sequence (VH) (AAQ13110) coding for the variable domain of a
CC human antibody heavy chain (HuVhlys), a ribosome binding site (RBS),
CC a second leader sequence (P2) (AAQ13099), and a sequence (VL)
CC (AAQ13111) coding for the variable domain of a human antibody light
CC chain (HuVllys). TAG sequences are represented in AAQ13108-09.
CC The libraries may be used to isolate clones producing specific
CC antibodies or antigen-binding antibody fragments by screening with
CC specific antigens.
XX
SQ Sequence 407 BP; 98 A; 111 C; 104 G; 94 T; 0 other;

```

alignment\_scores:

Quality: 388.50 Length: 121

Ratio: 3.847 Gaps: 1

Percent Similarity: 83.471 Percent Identity: 62.810

alignment\_block:

US-09-786-015-2 x AAQ13110 ..

Align seq 1/1 to: AAQ13110 from: 1 to: 407

```

1  GlnValGlnLeuGlnGlnSerGlyProSerLeuValLysProSerGlnTh 17
    |||
22  CAGGTCCAACTGACGAGAGCGGTCACGCTCTGTGAGACTGACCCAGAC 71
    |||
17  rLeuSerLeuThrcysThrValSerGlyPheSerLeuThrLysGlyGly 34
    |||
72  CCGTGGCTGACCTGCACCGTGTGCTGCTCACCCTGACGGCTATGCTG 121
    |||
34  alserTPValArgGlnAlaProGlyLysAlaLeuGlnTTPLeuGlyGly 50
    |||
122  TAAACTGGTGAGACACCCACCTGAGAGGCTCTGAGTGATGGATG 171
    |||
51  ValSerSerGlyAlaLeuThrAlaTyrAsnThrAlaLeuGlnSerArgLe 67
    |||
172  ATTGGGGTGATGGAACACAGACTATTAATTCAGCTCTCAATCCAGAGT 221
    |||
67  uSerValThrArgAspThrSerLysSerGlnPheSerLeuSerLeuSer 84
    |||
222  GACAAATGCTGTGAGACACAGCAAGCAAGTTCAGCTGAGACTGACGA 271
    |||
84  erValThrThrGluAspThrAlaIleTyrTyrCysAlaLysSerValAsn 100
    |||
272  GCGTGACAGCCGCCGACACCGGCTATTATTGTGCAAGAGAGAGATG 321
    |||
322  .....TAPAGCTTGACTACTGCGGGGTGACGGCTCCCTCGT 356
    |||
101  GLYAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
    |||
117  uThrValSerSer 121
    |||
357  CACAGTCTCCTCA 369
    |||

```

seq\_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AAAT34095

seq\_documentation\_block:

ID AAT34095 standard; DNA; 357 BP.

XX AAT34095;

AC 12-OCT-1996 (first entry)

XX

DT

XX

```

DE  NEMM humanised 2B6 antibody heavy chain variable region DNA.
XX
XX
KW  Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW  Interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;
KW  atopic dermatitis; therapy; diagnosis; heavy chain; VH;
KW  monoclonal antibody; Mab; ss.
XX
OS  Synthetic.
XX
PN  WO9621000-A2.
XX
PD  11-JUL-1996.
XX
PF  22-DEC-1995; 95MO-US17082.
XX
XX  06-JUN-1995; 95US-0470110.
PR  23-DEC-1994; 94US-0363131.
PR  06-JUN-1995; 95US-0467420.
XX
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
PA  (SMIK ) SMITHKLINE BEECHAM PLC.
PI  Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
PI  Holmes SD, McMillan LJ, Thelsen TW.
XX  WPI: 1996-333976/33.
XX  P-PSDB: AAR98492.
XX
PT  New monoclonal antibody to human interleukin-5 - used to produce
PT  products for the treatment and diagnosis of conditions associated
PT  with excess eosinophil prodn., e.g asthma etc.
XX
XX  Example 4; Page 86-87; 120pp; English.
XX
XX  A synthetic DNA sequence (AAT34095) codes for the heavy chain variable
CC  region (AAR98492) of NEMM humanised antibody 2B6, comprising
CC  complementarity determining regions (see also AAR98460-82) derived from
CC  murine monoclonal antibody 2B6 VH (see also AAR98478) and framework
CC  regions from human immunoglobulin NMV, but with amino acid
CC  substitutions made at framework residues that might influence CDR
CC  presentation. A synthetic variable light chain sequence (AAT34096)
CC  was also constructed. Humanised 2B6 (see also AAT34093-94) is
CC  specific for human Interleukin-5 (IL-5) and can be used for the
CC  diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,
CC  allergic rhinitis and atopic dermatitis.
XX
XX  Sequence 357 BP; 82 A; 103 C; 98 G; 74 T; 0 other;
SO

```

```

151 AATATGGCGTAGTGGAGGCACACATTATATATTCGGCTCTCAGTCCAGACT 200
67 uSerValThrArgAspPthSerLysSerGlnPheSerLeuSerLeuSerS 84
|||||: :|||||:|||||:||||| 11111
|||||: :|||||:|||||:||||| 11111
201 GAGTATAGTGAAGAACAACAGCAGACAGAGCTGACCTGAGACTCAGCA 250
84 eValThrThrGlnuSpThrAlaIleTyrTyrCysAluLysSerValasn 100
|||||: :|||||:|||||:|||||:|||||: :||
251 GCGTACACACCCCGACACACCGGGCTCTATTACTGTGCTCG:....GAT 294
101 GtAspSerValProTyrGlyLeuAspTyrTrpSerProGlyLeuLeu 117
295 CCCCCCTTCTCTCTACTACTAGCGCTTACTACTACGTGGGACAAAGTACCAGGT 344
117 uThrValSerSer 121
:|||||:|||||
345 CACCGTCTCGAC 357

seq_name: /SIBS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:AAQ31365
seq_documentation_block:
ID AAQ31365 standard; DNA; 438 bp.
XX
AC AAQ31365;
XX
DT 30-MAR-1993 (first entry)
XX
DE pUC-RVh-PM1f-4.
XX
KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KM complementarily determining region; mouse; monoclonal; hybrido-
XX plasmid; polymerase chain reaction; amplify; ss.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 12..425
FT FT /*tag= a
FT FT 12..68
FT FT /*tag= b
FT mat_peptide 69..425
FT /*tag= c
XX
XX WO9219759-A.
XX
XX 12-NOV-1992.
XX
XX 24-APR-1992; 92WO-JP00544.
XX
XX 25-APR-1991; 91JP-0095476.
XX
XX 19-FEB-1992; 92JP-0032084.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
XX
XX WPI: 1992-398882/48.
XX
XX P-PSDB: AAR29014.
XX
XX Reconstituted human antibody to human Interleukin-6 receptor -
XX has low antigenicity and contains mouse V-region complementarity
XX determining regions
XX
XX Disclosure; Page 142-3; 207pp; Japanese.
XX
XX The sequences given in AAQ31360-61 and AAQ31365-66 are plasmids encoding
XX portions of monoclonal antibodies which were derived from mouse
XX hybridomas. The DNA encoding complementarity determining regions
XX (CDR's) was isolated by polymerase chain reaction. The antibodies
XX produced recognises human interleukin-6 receptor (IL-6R). The
XX hybridoma cells were transformed with plasmids containing fragments
XX of the antibody gene which caused the production of the antibody from
XX the hybridoma cells.

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